

Delaval, Jan

91996 + 92523

From: Huynh, Phuong N.
Sent: Tuesday, April 22, 2003 8:48 AM
To: Delaval, Jan
Subject: RE: RE: 09/674,716

Good morning Jan,
The correct USSN is 09/674,716. Sorry about that. How are you doing otherwise? Neon.

-----Original Message-----

From: Delaval, Jan
Sent: Tuesday, April 22, 2003 7:10 AM
To: Huynh, Phuong N.
Subject: RE: RE: 09/555,964

no CRF for this case number

http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09555964

-----Original Message-----

From: Huynh, Phuong N.
Sent: Monday, April 21, 2003 1:37 PM
To: Delaval, Jan
Subject: RE: 09/555,964

Jan,

Please search peptides of SEQ ID NO: 3, 5, 7, 9, 11, 13, 1, 2, 17, 18 against commercial and interference databases.

Thanks,
Neon
Art unit 1644
Mail 9E12
Tel 308-4844

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Access DB# 91996

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN <input checked="" type="checkbox"/>
Searcher Phone #: <u>4448</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: <u>4120103</u>	Structure (#) <input checked="" type="checkbox"/>	Questel/Orbit _____
Date Searcher Picked Up: <u>4/26/03</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>60</u>	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>120</u>	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 828.199 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415

Sequence: 1 aaagctttacagttactcagc.....tggggccaagggacactagt 415

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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GenEmbl:
1: gb_ba:
2: gb_hgt:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
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22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:
28: em_un:
29: em_vi:
30: em_hgt_hum:
31: em_hgt_inv:
32: em_hgt_other:
33: em_hgt_mus:
34: em_hgt_pln:
35: em_hgt_rod:
36: em_hgt_mam:
37: em_hgt_vrt:
38: em_sy:
39: em_hgt_hum:
40: em_hgt_mus:
41: em_hgt_other:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	415	100.0	415	6	AX010600	AX010600 Sequence
2	415	100.0	415	6	AX010643	AX010643 Sequence
3	310.6	74.8	1658	10	BC031470	BC031470 Mus muscu
4	310.4	74.8	403	6	AX080317	AX080317 Sequence
5	295.6	71.2	403	10	MMU05819	U05819 Mus musculu
6	295.2	71.1	477	10	AB050074	AB050074 Mus muscu
7	292.6	70.5	399	10	MUSIGHFZX	M17726 Mouse Ig fa
8	289.8	69.8	396	10	MUSIGHRT	AJ223543 Mus muscu
9	289	69.6	314	10	MUSIGHRT	M32044 Mouse Ig ac
10	288	69.4	314	10	MUSIGHRU	M32045 Mouse Ig ac
11	287.4	69.3	314	10	MUSIGHRW	M32047 Mouse Ig ac
12	286.4	69.0	208357	2	AC073590	AC073590 Mus muscu
13	284.4	68.5	313	10	MUSIGHRY	M32049 Mouse Ig ac
14	284.2	68.5	314	10	MUSIGHRX	M32048 Mouse Ig ac
15	283.8	68.4	345	10	MMIGM18	X76014 Mus musculu
16	283.2	68.2	306	10	MUSIGHRV	M32046 Mouse Ig ac
17	281	67.7	314	10	MUSIGHRZ	M32050 Mouse Ig ac
18	278.6	67.1	414	10	MUSIGHAA2	M59922 Mouse Ig he
19	278.6	67.1	417	10	MUSIGHAAL	M59921 Mus musculu
20	278.4	67.1	305	10	MUSIGHSA	M32051 Mouse Ig ac
21	277.2	66.8	318	10	MMHCVR	X66664 M.musculus
22	273.6	65.9	375	10	AY090914	AY090914 Mus muscu
23	273.4	65.9	417	10	MUSIGHBMA	M98041 Mouse Ig re
24	272.4	65.6	300	10	MMIGVH22	X03398 Mouse gene
25	272	65.5	357	6	E15671	E15671 DNA encodin
26	271.2	65.3	345	10	AF132844	AF132844 Mus muscu
27	270.4	65.2	363	10	MUSIGKCLI	M15232 Mouse IGM r
28	269.4	64.9	403	6	AR022572	AR022572 Sequence
29	269.4	64.9	403	6	AR037587	AR037587 Sequence
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31	269	64.8	351	10	AY090913	AY090913 Mus muscu
32	268.8	64.8	351	10	S73907	S73907 Ig V kappa
33	268.6	64.7	427	10	MUSIGHHT	M17167 Mouse Ig mu
34	268.4	64.7	351	10	AF242213	AF242213 Mus muscu
35	268.4	64.7	376	10	MUSBRE3A	L13846 Mouse antib
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37	267.8	64.5	360	6	AR108682	AR108682 Sequence
38	267.2	64.4	354	10	MMU73591	U73591 Mus musculu
39	266.8	64.3	185591	2	AC073561	AC073561 Mus muscu
40	266.8	64.3	208357	2	AC073590	AC073590 Mus muscu
41	266.2	64.1	1515	9	S65761	S65761 anti-colore
42	265.6	64.0	345	10	AF178605	AF178605 Mus muscu
43	265.6	64.0	345	10	AF178606	AF178606 Mus muscu
44	265.6	64.0	345	10	AF178607	AF178607 Mus muscu
45	265.6	64.0	357	10	MMHCVRL0	X90885 M.musculus

ALIGNMENTS

RESULT 1
AX010600
LOCUS AX010600
DEFINITION Sequence 1 from Patent WO9958679.
ACCESSION AX010600
VERSION AX010600.1 GI:9997411
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 415)
Bonnefoy J.Y., Crowe S.J., Rapson N.T., Ellis J.H. and Shearin J.
Antibodies to cd23, derivatives thereof, and their therapeutic uses
Patent: WO 9958679-A 1 18-NOV-1999

DNA llinear PAT 06-SEP-2000

BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source

Location/Qualifiers
1. .415
/organism="Mus musculus"
/db_xref="taxon:10090"
<3...>413
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC07526.1"
/db_xref="GI:9997412"
/translation="ALOLLSTODLMDLFLFFIVLLKGVSEVKLESGGLVQPGG
SKLSCVAGFTFSCYKWSWVROSPKEGLEWAEIRLKSNDVATHYAESVKGKFTISR
DQSKRLYLQMSLRAESGVYCTDFDWMGGTL"

CDS

BASE COUNT 111 a 76 c 110 g 118 t

Query Match 100.0%; Score 415; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.9e-113;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTAA 60
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Db 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGG 120
Qy 121 TGCACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTTTCAGTGGCT 180
Db 121 TGCACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTTTCAGTGGCT 180
Qy 181 ACTGGATCTCTGGTCCGACGCTCCACAGAGAGGGCTTGAGTGGTTCGCTGAAATTA 240
Db 181 ACTGGATCTCTGGTCCGACGCTCCACAGAGAGGGCTTGAGTGGTTCGCTGAAATTA 240
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Db 241 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAGGGAAGTTCCACCA 300
Qy 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
Db 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
Qy 361 ACAGTGGAGTTTATTACTGTACAGATTTTCATAGCTGGGCGCCAAAGGACACTAGT 415
Db 361 ACAGTGGAGTTTATTACTGTACAGATTTTCATAGCTGGGCGCCAAAGGACACTAGT 415

RESULT 2
AX010643/c
LOCUS AX010643 415 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 46 from Patent WO9958679.
ACCESSION AX010643
VERSION AX010643.1 GI:9997452
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 415)

REFERENCE
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 46 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source

Location/Qualifiers
1. .415
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 118 a 110 c 76 g 111 t

Query Match 100.0%; Score 415; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.9e-113;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTAA 60
Db 415 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTAA 356
Qy 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGG 120
Db 355 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGG 296
Qy 121 TGCACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTTTCAGTGGCT 180
Db 295 TGCACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTTTCAGTGGCT 236
Qy 181 ACTGGATCTCTGGTCCGACGCTCCAGAGAGGGCTTGAGTGGTTCGCTGAAATTA 240
Db 235 ACTGGATCTCTGGTCCGACGCTCCAGAGAGGGCTTGAGTGGTTCGCTGAAATTA 176
Qy 241 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAGGGAAGTTCCACCA 300
Db 175 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAGGGAAGTTCCACCA 116
Qy 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
Db 115 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 56
Qy 361 ACAGTGGAGTTTATTACTGTACAGATTTTCATAGCTGGGCGCCAAAGGACACTAGT 415
Db 55 ACAGTGGAGTTTATTACTGTACAGATTTTCATAGCTGGGCGCCAAAGGACACTAGT 1

RESULT 3
BC031470
LOCUS BC031470 1658 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, Similar to immunoglobulin heavy chain 1 (serum Ig2a), clone MGC:25748 IMAGE:3991558, mRNA, complete cds.
ACCESSION BC031470
VERSION BC031470.1 GI:21594582
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1658)
REFERENCE Strausberg,R.
AUTHORS Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 30 Row: h Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

FEATURES

source
1. .1658
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
/clone="MSC:25748 IMAGE:3991558"
/tissue_type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMIV."
/clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
54...1448
CDS
/codon_start=1
/product="similar to immunoglobulin heavy chain 1 (serum IgG2a)"
/protein_id="AAH31470.1"
/db_xref="GI:21594583"
/translation="MDLRSCARIIIVLLKGVQSEVVKLEESGGGLVQPGSMKLSCLVAS
GFTESNMWVRQSPKLEWVAQIRLSDNTATHYAESVKGRFTISRDDSKRLYL
QMSLRADGIYCTNADYWGQTSVTVSSAKTAPSYVPLAPVCGDPTGSSVTIG
CLVKGYPEPVTITWNSGLSSGVHTFPAYLDLXTLSSSVTVSTWPSQSTICNV
AHPASSKYDDKIEPRGPTIKPCPKCAPNLLGGPSVFIPPKIKDVLIMISLSPW
TCVVVDYSEDPPVQISWENNVVLTAQTHREDYNSTLRVSKALPIQHDQMSK
EFLKVNKALPAPIERTISKPGSVAPQVYVLPPEEBEMTKKQVTLICMVDTPPE
LHIVWNTNKGTELEUNYKTEPFVLDSDGSYFMYSLRVERKANWVERNSYCSVVHEGLH
NHHYTFSTFSTPGK"
BASE COUNT 534 a 421 c 367 g 336 t
ORIGIN

Query Match 74.8%; Score 310.6; DB 10; Length 1658;
Best Local Similarity 87.4%; Pred. No. 5.6e-82;
Matches 340; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 8 ACAGTTACTACACACAGAGACTCACCATGGATTTTGGGCTGATTTTATTTATTTTCT 67
DB 32 ACACGGACACAGAACATTCACATGGACTTGAGACTGAGCTGTCTTTATTATTGTCT 91
QY 68 TTTAAAGGGTCCAGATGAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACAC 127
DB 92 TTTAAAGGGTCCAGATGAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACAC 151
QY 128 TGGAGATCCATGAACCTCTCTGTAGCTCTGATTTTCTGATTTTCTGATTTTCTGAT 187
DB 152 TGGAGATCCATGAACCTCTCTGTAGCTCTGATTTTCTGATTTTCTGATTTTCTGAT 211
QY 188 GTCTTGGTCCGCGAGTCTCCAGAGAAGGGCTTCAGTGGTGTGCTGAAATAGATTGAA 247
DB 212 GAACGTGGTCCGCGAGTCTCCAGAGAAGGGCTTCAGTGGTGTGCTGAAATAGATTGAG 271
QY 248 ATCTGATATATGACACACATTTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 307
DB 272 ATCTGATATATGACACACATTTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 331
QY 308 AGATGATCCAAAGTCGCTTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGG 367
DB 332 AGATGATCCAAAGTCGCTTACCTGCAATGAACAGCTTAAGAGGCTGAAGACAGTGG 391
QY 368 AGTTTATTACTACAGATTTTCATAGACT 396
DB 392 AATTATTACTACAAATGCTATGGACT 420
RESULT 4
AX080317
LOCUS 453 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 14 from Patent WO0105427.
ACCESSION AX080317
VERSION AX080317
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 453)
AUTHORS Reiter,R., Witte,O., Safran,D.C. and Jakobovits,A.
TITLE Psca: prostate stem cell antigen and uses thereof
JOURNAL Patent: WO 0105427-A 14 25-JAN-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US) ; Urogenesys, Inc.
(US)
FEATURES Location/Qualifiers
source 1. .453
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="MONOCLONAL ANTIBODY 2H9"
BASE COUNT 115 a 93 c 122 g 123 t
ORIGIN
Query Match 74.8%; Score 310.4; DB 6; Length 453;
Best Local Similarity 92.6%; Pred. No. 6.1e-82;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTGA 94
DB 6 CTTGGGTTGAGCTGGGTTTTTATTGTTCTTTTAAAGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGACTCTGGAGAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCCTGTGT 154
DB 66 GCTTGAGGACTCTGGAGAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCCTGTGT 125
QY 155 AGCCTCTGGATTTACTTTCAGTGGCTAGTGTCTTGGTCCGCGAGTCTCCAGAGAA 214
DB 126 AGCCTCTGGATTTACTTTCAGTAAATTAAGTGTGCTGGTCCGCGAGTCTCCAGAGAA 185
QY 215 GGGCTTGAGTGGTTCCTCAAAATAGATTGAAATCTGTAATATGACACATATGTC 274
DB 186 GGGCTTGAGTGGTTCCTCAAAATAGATTGAAATCTGTAATATGACACATATGTC 245
QY 275 GGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 334
DB 246 GGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 305
QY 335 GCAATGAACAGCTTAAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 386
DB 306 GCAATGAACAGCTTAAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 357
RESULT 5
MMU05819
LOCUS 405 bp mRNA linear ROD 22-FEB-1994
DEFINITION Mus musculus BALB/c Ig mu heavy chain V-JH2 region mRNA, partial cds.
ACCESSION U05819
VERSION U05819.1 GI:456279
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 405)
AUTHORS Yong,F.J., Chan,S. and Ren,E.
TITLE Identification of a new VH J606 family member utilized in the murine immune response to Hepatitis B surface antigen
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 405)
AUTHORS Ren,E.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1994) Ee-Chee Ren, Microbiology and W.H.O. Immunology Center, National University of Singapore, Faculty of Medicine, Singapore. 0511, Republic of Singapore
FEATURES Location/Qualifiers
source 1. .405
/organism="Mus musculus"
/strain="BALB/c"


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FEATURES          Location/Qualifiers
source            1..314
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                 /db_xref="taxon:10090"
intron            <1..11
                 /note="Ig H-chain V-region intron"
exon              12..>314
                 /note="Ig H-chain V-region, X"
BASE COUNT       88 a 58 c 86 g 82 t
ORIGIN            Chromosome 12.

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Best Local Similarity 95.2%; Pred. No. 1.5e-75;
Matches 298; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 76 GGGTCCAGAGTGAAGCTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGAT 135
Db 2 GGGTCCAGAGTGAAGCTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGAT 61

QY 136 CCATGAAACTCTCCTGTAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 195
Db 62 CCATGAAACTCTCCTGTGTGCTCTGGATTACATTTTCAGTAACTACTGGATGACTGGG 121

QY 196 TCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 255
Db 122 TCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 181

QY 256 ATTATGCAACACATTATGCGAGTCTGTGAAAGGAACTTCACCATCTCAAGAGATGATT 315
Db 182 ATTATGCAACACATTATGCGAGTCTGTGAAAGGAGGTTTCCACCATCTCAAGAGATGATT 241

QY 316 CCAAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGATGAGTTTATT 375
Db 242 CCAAAAGTAGTGTCTACCTGCAAAATGAACAGCTTAAGGCTGAAGACACTGGAATTTATT 301

QY 376 ACTGTACAGATTT 388
Db 302 ACTGCACAGATCT 314

RESULT 11
MUSIGHRW
LOCUS            Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma
DEFINITION
ACCESSION       M32047.1 GI:195972
VERSION
KEYWORDS        V-region; immunoglobulin heavy chain; processed gene.
SOURCE          Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 68.2C4.
ORGANISM        Mus musculus
REFERENCE
AUTHORS         Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE           Mouse antibody response to group A streptococcal carbohydrate
JOURNAL         J. Immunol. 143 (12), 4213-4220 (1989)
MEDLINE         90079033
PUBMED          2512352
FEATURES
source          Location/Qualifiers
                 1..314
                 /organism="Mus musculus"
                 /db_xref="taxon:10090"
intron          <1..11
                 /note="Ig H-chain V-region intron"
exon            12..>314
                 /note="Ig H-chain V-region, X"
BASE COUNT      89 a 57 c 84 g 84 t
ORIGIN          Chromosome 12.

Query Match      69.3%; Score 287.4; DB 10; Length 314;
Best Local Similarity 94.9%; Pred. No. 4.6e-75;
Matches 297; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 76 GGGTCCAGAGTGAAGCTTGAAGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGAT 135
Db 2 GGGTCCAGAGTGAAGCTTGAAGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGAT 61

QY 136 CCATGAAACTCTCCTGTAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 195
Db 62 CCATGAAACTCTCCTGTGTGCTCTGGATTACATTTTCAGTAACTACTGGATGACTGGG 121

QY 196 TCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 255
Db 122 TCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 181

QY 256 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAACTTCACCATCTCAAGAGATGATT 315
Db 182 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAGGTTTCCACCATCTCAAGAGATGATT 241

Query Match      69.4%; Score 288; DB 10; Length 314;
Best Local Similarity 94.9%; Pred. No. 3e-75;
Matches 297; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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ORIGIN		Chromosome 12.									
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RESULT 14											
MUSIGHRX											
LOCUS											
DEFINITION											
Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma											
65.1B3, partial cds.											
VERSION											
M32048.1 GI:195973											
KEYWORDS											
V-region; immunoglobulin heavy chain; processed gene.											
SOURCE											
Mouse (Strain A/J), cDNA to mRNA, anti-GAC hybridoma 65.1B3.											
ORGANISM											
Mus musculus											
REFERENCE											
1 (bases 1 to 314)											
AUTHORS											
Jarvis,C.D., Cannon,L.E. and Stavnezer,J.											
TITLE											
Mouse antibody response to group A streptococcal carbohydrate											
J. Immunol. 143 (12), 4213-4220 (1989)											
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QY 330 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAG 384
Db 241 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAAATTTATTACTGTACAG 295

Search completed: April 26, 2003, 06:31:00
Job time : 871.449 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 549.077 Seconds

(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415

Sequence: T aagtttacagtactacgc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:**

2: em_estham:**

3: em_estin:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: gb_gss:**

18: em_gss_hum:**

19: em_gss_inv:**

20: em_gss_pln:**

21: em_gss_vrt:**

22: em_gss_fun:**

23: em_gss_mam:**

24: em_gss_mus:**

25: em_gss_othr:**

26: em_gss_pro:**

27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	286.2	69.0	375	10	BB842048
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8	273.4	65.9	597	9	AA472093
9	266	64.1	625	17	BH021344
10	247.4	59.6	615	10	BE288134
11	244.4	58.9	713	13	BG967386
12	223	53.7	904	12	BF133700
13	218.8	52.7	938	13	BG967834
14	209	50.4	522	10	AM401500
15	207.4	50.0	446	10	AW504516
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17	207.4	50.0	881	12	BG754897
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26	197.6	47.6	430	10	AW402433
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29	195.8	47.2	700	12	BG757291
30	195.2	47.0	516	10	AW402430
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33	193.6	46.7	663	10	BB586011
34	193	46.5	693	12	BG684987
35	193	46.5	866	14	BQ707524
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37	192.4	46.4	896	14	BQ715221
38	191.4	46.1	626	14	BM818875
39	191	46.0	864	13	BM008425
40	190.8	46.0	567	14	BQ266826
41	190	45.8	650	12	BF579925
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43	189.4	45.6	693	13	BG965016
44	188.6	45.4	635	12	BG398259
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ALIGNMENTS

RESULT 1
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LOCUS 601772396F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991558 5',
DEFINITION mRNA sequence.
ACCESSION BF163883
VERSION BF163883.1 GI:11044161
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAM9204 row: p column: 23
High quality sequence stop: 679.
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Library constructed by Life Technologies. Investigator
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BASE COUNT

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Best Local Similarity 90.8%; Pred. NO. 4.8e-60;
Matches 327; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

37 TGGATTTTGGCGTGATTTTATTTATTTGTTCTTTAAAAGGGGTCCAGAGTGAAGTGAAGC 96

Db 60 TTGAGACTGAGCTGTGCTTTTATTATGTTCTTTTAAAGGGGTCCACAGTGAAGTGAAGC 119

[illegible]

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Qy 217 GGCTTGAGTGGGTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACATTATGCGG 276

Db 239 GCGTTGAGTGGGTGCTCAAATTAGATTGAGATCTGATAATTATGCAACACATTATGGCG 298

Qy 277 AGTCTGTGAAGGGAAGTTTCACCATCTCAAGAGATGATTCAAAAGTCGTCTCTACCTGC 336

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RESULT 2
BB842048

[illegible]

ACCESSION BB842048
VERSION BB842048.1 GI:17042779

KEYWORDS EST.
SOURCE house mouse.

ORGANISM	MUS MUSCULUS
REFERENCE	1 (bases 1 to 375)
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 375)

AUTHORS

AKMURA, T., ARAKAWA, T., CARINCI, P., FURUKO, M., HANAGAKI, K., ISHII
HAYASU, N., HIRAMOTO, K., HIRAKOTA, T., HIROZANE, T., IMOTANI, K., ISHII
Y., ITO, M., KAWAI, J., KOJIMA, Y., KONNO, H., KOUDA, M., MATSUYAMA, T.,
NAKAMURA, M., NISHI, K., NOMURA, K., NUMASAKI, R., OKAZAKI, Y., OKIDO, T.,
SAITO, R., SAKAI, C., SAKAI, K., SAKAZUME, N., SASAKI, D., SATO, K.,
SHIBATA, K., SHINGAWA, A., SHIRAKI, T., SOGABE, Y., SUZUKI, H., TAGAWA
A., TAKAHASHI, F., TAKAKU-AKIHARA, S., TANAKA, T., TOMARU, A., TOYA, T.,
WATAHAKI, A., YASUNISHI, A., YAMAMOTO, M., AND HAYASHIZAKI, Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

JOURNAL	COMMENT
Unpublished (2001)	<p>Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan</p>

Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
waji, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001).

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

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FEATURES
source
e mouse
tissues.
Location/Qualifiers
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/strain="C57BL/6J"
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 embryos from unfertilized egg to blastocyst, embryonic
 part of E7.5 embryos, extraembryonic part of E7.5 embryos
 and E12.5 female mesonephros/gonad) and one newborn
 ovary cDNA library. Average insert size 1.5 kb. All
 source libraries are cloned unidirectionally with Oligo(dT)
)-Not primers. References include: (1) Genome-wide
 expression profiling of mid-gestation placenta and embryo
 using a 15,000 mouse developmental cDNA microarray, 2000,
 Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
 Large-scale cDNA analysis reveals phased gene expression
 patterns during preimplantation mouse development, 2000,
 Development, 127: 1737-1749; (3) Genome-wide mapping of
 unselected transcripts from extraembryonic tissue of
 7.5-day mouse embryos reveals enrichment in the t-complex
 and under-representation on the X chromosome, 1998, Hum
 Mol Genet 7: 1967-1978."

BASE COUNT	107 a	69 c	99 g	100 t
ORIGIN				

Query Match 69.0%; Score 286.2; DB 10; Length 375;
Best Local Similarity 88.0%; Pred. No. 1.6e-57;
Matches 323; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

QY 8 ACAGTTACTACGACACAGGACCTCACCATTGGATTTTGGGCTGATTTTTTTATTGTTCT 67

Db 10 ACAGGACACAGAACATTCACCATGGACCTGAGACTGAGCTGCTGCTTTTATTATTCTCT 69

Qy 68 TTTAAAGGGGTCACAGTGAAGTGAAGCTTGAGGAGCTTGGTGGCAACC 127

Db 70 TTTAAAGGGGTCCAGAGTGAAGTGAAGCTTCGAGGAGCTCGAGGAGGCTTGGTGCAACC 129

QV 128 TGGAGGATCCATGAAGACTCTCTCTGTGTAGGCTCTGGATTTACTTTTCATGTGGCTACATGGAT 167

DP 130 TGGAGGAT-CATGAAGACTCTCTCTGTGTAGGCTCTGGATTCATTTTCAGTAAGTAACTGGAT 188

188 GTCCTGGTCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTGCTGAATTAGATTGAA 247

Db 144 TCACTAAGTACTACATGAACCTGGGTCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG 203

Qy 232 CTGAATTTAGATTGAATCTGATTAATATGCAACACACATTAATGCGGAGTCTGTGAAGGGA 291

Db 204 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTAATGCGGAGTCTGTGAAGGGA 263

Qy 292 AGTTCAACATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 351

Db 264 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 323

Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCATAGACTGGGGCCAAAG 406

Db 324 GAGTTGAAGACACTGGCATTTATTACTGTACCGAGCTGGGTTTGCCTTACTTGGGGCCAAAG 383

Qy 407 GACACTAGT 415

Db 384 GACTCTGCT 392

RESULT 5

BC011342

LOCUS

DEFINITION Mus musculus, clone IMAGE:3992829, mRNA.

ACCESSION BC011342

VERSION BC011342.1 GI:15030173

KEYWORDS HTC.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapsb-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 23 Row: n Column: 19

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein

This clone has the following problem: incomplete processing.

Location/Qualifiers

1. .1526

/organism="Mus musculus"

/db_xref="taxon:10090"

/map="C57BL/6J"

/clone="IMAGE:3992829"

/tissue_type="Mammary old, gross tissue."

/clone_lib="NCL CGAP_Mam5"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

374 a 412 c 389 g 351 t

BASE COUNT

ORIGIN

Query Match 68.4%; Score 284; DB 11; Length 1526;

Best Local Similarity 87.6%; Pred. No. 4.9e-57;

Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

Qy 52 TTTTCTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111

Db 35 TATTCATAGTTTTTCTCTTTAAAGGTTGCCAGAGTCAAGTGAAGTTTGAGTAGTCTGGAG 94

Qy 112 GAGGCTTGTCGCAACCTCGAGGATCCATGAACCTCTCCTGTGTAGCCTCTGATTTACTTT 171

Db 95 GAGGCTTGTCGCAACCTCGAGGATCCATGAACCTCTCCTGTGTAGCCTCTGATTTACTTT 154

Qy 172 TCAGTGGTACTGGATGTTCTTGGGTCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG 231

Db 155 TCACTAACTACTACATGAACCTGGTCCGCCACTCTCCAGAGAAGGGGCTTGAGTGGGTTG 214

Qy 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATCGGAGTCTGTGGAAGGGA 291

Db 215 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATCGGAGTCTGTGGAAGGGA 274

Qy 292 AGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 351

Db 275 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 334

Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCATAGACTGGGGCCAAAG 405

Db 335 GAGTTGAAGACACTGGCATTTATTACTGTACCGAGCTGGGTTTGCCTTACTTGGGGCCAAAG 394

Qy 406 GGACACTAGT 415

Db 395 GGACTCTGCT 404

RESULT 6

BB842247

LOCUS

DEFINITION BB842247 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430004H07 5', mRNA sequence.

ACCESSION BB842247

VERSION BB842247.1 GI:17042978

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp

URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES

Location/Qualifiers
 1. 367
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="F430004H07"
 /clone_lib="RIKEN full-length enriched, 6 days neonate spleen"
 /tissue_type="spleen"
 /dev_stage="6 days neonate"
 /note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
 Mol Genet 7: 1967-1978."

 BASE COUNT 105 a 68 c 98 g 96 t
 ORIGIN

Query Match 67.0%; Score 278.2; DB 10; Length 367;
 Best Local Similarity 87.7%; Pred. No. 1.3e-55;
 Matches 315; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
 QY 8 ACAGTTACTCAGCACAGGACCTCACCATGGATTTTGGGCTGATTTTTTTATTGTTCT 67
 DB 10 ACAGGACAAAGAACATTCACCATGGACTTGAGACTGAGCTGTGCTTTATTGTTCT 69
 QY 68 TTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGCTTGAGAGGGCTTGTCGAACC 127
 DB 70 TTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGCTTGAGAGGGCTTGTCGAACC 129
 QY 128 TGGAGGATCATGAACCTCTCCTGTAGCTCTGGAATTTACCTTTCAGTGGCTACTGGAT 187
 DB 130 TGGAGGATCATGAACCTCTCCTGTGCTCTGGAATTTACCTTTCAGTGGCTACTGGAT 188
 QY 188 GTCTTGGTCCGCGAGTCTCCAGAGAAGGGCTTGAGTGGGTGCTGCAATTAGATTGAA 247
 DB 189 GAATGGGTCCGCGAGTCTCCAGAGAAGGGCTTGAGTGGGTGCTGCAATTAGATTGAA 248
 QY 248 ATCTGATAATTATGCAACATTTATCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAG 307
 DB 249 ATCTGATAATTATGCAACATTTATCGGAGTCTGTGAAAGGAGGTTTACCACTCAAG 308
 QY 308 AGATGATTCGAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTG 366
 DB 309 AGATGATTCGAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTG 367

RESULT 7

BF581663
 LOCUS 602099628F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219447 5', mRNA linear EST 12-DEC-2000
 DEFINITION mRNA sequence.
 ACCESSION BF581663
 VERSION BF581663.1 GI:11655375
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 560)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAN9801 row: h column: 08
 High quality sequence stop: 555.
 Location/Qualifiers
 1. 560
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4219447"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 152 a 128 c 133 g 147 t
 ORIGIN

Query Match 66.6%; Score 276.2; DB 12; Length 560;
 Best Local Similarity 90.0%; Pred. No. 3.6e-55;
 Matches 307; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
 QY 52 TTTTITTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 82 TATTCATAGTTTTTCTCTTAAAGGTGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 141
 QY 112 GAGGCTTGGTCAACCTCGAGGATCCATAACTCTCTGTCTAGCCCTCGATTACTT 171
 DB 142 GAGG-TTGGTCAACCTCGAGGATCCATAACTCTCTGTCTAGCCCTCGATTACTT 200
 QY 172 TCAGTGGCTACTGGATGCTTTGGGTCGCGAGTCTCCAGAGAAGGGGTTGAGTGGGTTG 231
 DB 201 TTAGCAACTACTGGATGACCTGGTCCGCGACTCTCCAGAGAAGGGGTTGAGTGGATTG 260
 QY 232 CTCGAATTTAGATTGAATCTGATAATTATGCAACACATTATCGCGAGTCTGTGAAGGGA 291
 DB 261 CTGAATTTAAATTTGACATCTGATAATTTTGCAACACATTATCGCGAGTCTGTGAAGGGA 320
 QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTTACCTGCAAAATGAACACTTAA 351
 DB 321 GGTTCACCATCTCAAGAGATGATTCCAAAGTAGTGTCTTACCTGCAAAATGAACACTTAA 380
 QY 352 GAGCTGAACAGAGTGGAGTTTATTACTGTACAGATTTTCATA 392
 DB 381 GAGCTGAACAGACTGGCTTTTATTACTGTACGGGTCTACTA 421

RESULT 8

QY	153	GTAGCCTCTGGATTACTTTCAGTGGCTACTGGATGCTTTGGGTCCGCCAGTCTCCAGAG	212		
Db	61	GTTCCTCTGGATTCACTTTTCAGTAACTACTGGATGAACCTGGTGGCCAGTCTCCAGAG	120		
QY	213	AAGGGCTCTGAGTCGGTGGCTGAAATAGATGTTGAAATCTGATATTTATGCAACACATTAT	272		
Db	121	AAGGGCTCTGAGTCGGTGGCTGAAATAGATGTTGAAATCTGATATTTATGCAACACATTAT	180		
QY	273	GCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTCTAC	332		
Db	181	GCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTCTAC	240		
QY	333	CTGCAATGACACAGCTTTAAGAGCTGGAACAGAGTGGAGTTTATTACTGTAC	382		
Db	241	CTGCAATGACACAGCTTTAAGAGCTGGAACAGAGTGGAGTTTATTACTGTAC	290		
RESULT 10					
LOCUS	BE288134	601095304F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489841 5'	linear EST 26-OCT-2000		
DEFINITION	mRNA sequence.				
ACCESSION	BE288134				
VERSION	BE288134.1	GI:9167624			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1. (bases 1 to 615)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8531 row: h column: 02 High quality sequence stop: 583.				
FEATURES	Location/Qualifiers				
source	1..615 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:3489841" /clone_lib="NCI_CGAP_Mam5" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DH10B"				
BASE COUNT	167 a	139 c	147 g 162 t		
ORIGIN					
Query Match	59.6%	Score 247.4;	DB 10; Length 615;		
Best Local Similarity	78.5%	Pred. No. 2.3e-48;			
Matches	296;	Conservative 0;	Mismatches 81; Indels 0; Gaps 0;		
QY	8	ACAGTTACTCAGACACACAGGACCGCTACCATCGAATTTGGCGCTGATTTTTTTTATTGTCT	67		
Db	19	AAAGTACACAGATCATTCATGTCATGTACTTGGACTGAGCTGTGATTCATGTTTTCT	78		
QY	68	TTTAAAGGGGTCGAGAGTGAAGTGAAGCTTTGAGAGGCTCTGGAGAGGCGTTGGTCAACC	127		

Db	79	CTTAAAGGTTGCAGTGTGAGGTGAACACTGGATGAGACTGGAGGAGGCTTTGGTGAACC	138
Qy	128	TGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTACTTTCAAGTGTGCTACTGGAT	187
Db	139	TGGAGGCCCATGAAACTCTCCTGTGTGTGCTCTGGATTCACTTTTGGTGAAGTACTGGAT	198
Qy	188	GTCTTTGGTCCGCGCAGTCTCCAGAGAAGGGCTGTGAGTGGGTGCTGAAATAGATTGAA	247
Db	199	GAATCGGTCGCGCAGTCTCCAGAGAAGGACTGGAGTGGGTATCACAATATAGAACAA	258
Qy	248	ATCTGATAATTATGCAACACATTTATGGGAGCTCTGTGAAAGGGAAGTTTCACCATCTCAAG	307
Db	259	ACCTTATAATTATGAACATATTTATTCAGATTCTGTGAAAGCGAGATTCACCATCTCAAG	318
Qy	308	AGATGATTCCAAAAGTCGTCTTACCTGCAATGAACAGCTTAAGAGCTGAAGACATGG	367
Db	319	AGATGATTCCAAAAGTGGTGTCTACTTGCATAATGAACAACCTTAAGACCTGAAGACATGG	378
Qy	368	AGTTTATTACTGTACAG	384
Db	379	TATCTATTATTGTACAG	395
RESULT 11			
LOCUS	BG967386	60283351AF1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988282 5',	linear EST 12-JUN-2001
DEFINITION	mRNA sequence.		
ACCESSION	BG967386		
VERSION	1 GI:14355023		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	NTH-MGC http://mgc.nci.nih.gov/ .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM11000 row: k column: 03 High quality sequence stop: 703. Location/Qualifiers 1. 713 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4988282" /clone_lib="NCI_CGAP_Co24" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: colon; Vector: pCMV-SPORT6; Site:1: NotI; site_2: SalI; Cloned unidirectionally. Primer: Oligo dt Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
BASE COUNT	185 a	168 c	181 g 179 t
ORIGIN	1		
Query Match	58.9%	Score 244.4;	DB 13; Length 713;
Best Local Similarity	85.3%;	pred. No. 1.le-47;	
Matches	285;	Conservative 0;	Mismatches 46; Indels 3; Gaps 1;
Qy	52	TTTTTTTATTGTCTTTTAAAGGGTCCAGAGTGAAGCTTGAAGCTTGAGAGTCTGGAG	111
Db	79	TATTCATAGTTTTCCTCTTAAAGGTGTCCAGAGTGAAGTGAAGCTTGAGAGTCTGGAG	138

Db	81	TATTTCATAGTTTTTCTCTTAAAGGCTCCAGAGTGAAGTGAAGCTTCAGGAGCTGGAG	140
Qy	112	GAGGCTTTGGTGCACACCTGGAGGATCCATGAACATCTCCTGTGTAGCCTCTGGATTACTT	171
Db	141	GAGGCTTTGGTGCACACCTGGAGGATCCATGAACATCTCCTGTGTAGGATTCACATT	200
Qy	172	TCAGTGGCTACTGATCTTTGGTCCGCCAGTCTCCAGAGAGGGGCTTTGAGTGGGTTG	231
Db	201	TCAGTAACCTACTGGATGAACCTGGGTCCGCCAGTCTCCAGAGAGGGGCTTTGAGTGGGTTG	260
Qy	232	CTGAAA---TTAGATTGAAATCTGATAATTA---TGCACACATTAATGCGAGGTCTCTGA	285
Db	261	CTGAAACTTACGATTGAACACTCTAACTAATTACTGCAACACATTAATGCGAGGTCTCTGA	320
Qy	286	AAGGGAAGTTCCACATCTCAGAGATG-ATTCCAAAGTCGTCTTACCTGCAAAATGAA	343
Db	321	AAGGGAAGTTCCACATCTCAGAGATGCATCCAAAACGATGTCCTACTGTCACATGAA	380
Qy	344	CAGCTTAA--GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATAGACT	396
Db	381	CAAGCTTTAAGCAGCCTCGAAGACTGGCATTTATTACTGTACAGAGGTTATGGACT	436

RESULT	14
AU401500	
LOCUS	522 bp mRNA linear EST 16-FEB-2000
DEFINITION	UT-HF-BKO-aau-b-08-0-Ul.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:	3055046 5', mRNA sequence.
ACCESSION	AW401500
VERSION	AW401500.1 GI:6920108
KEYWORDS	EST.
SOURCE	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITLE	Contact: Robert Strausberg, Ph.D. Email: crabosr@mail.nih.gov
JOURNAL	Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/brrp/image/image.html Seq primer: M13 Forward.

BASE COUNT	123 a	128 c	155 g	116 t	
ORIGIN					
Query Match		50.4 %	Score 209;	DB 10;	Length 522;
Best Local Similarity		76.0 %;	Pred No. 2,7e-39;		
Matches 273;	Conservative	0;	Mismatches 80;	Indels 6;	Gaps 1
QY 30	CTCACCATGGATTTGGGCT-----GATTTTTTTTTATGTCTCTTTTAAAGGGGTCCAG	83			

Db	70	CTCACATGGAGTTGGGCTGAGCTGGAATTCCTTCTGCTATTTTAAAGGTGTCGAG	129
Qy	84	AGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCATGA	143
Db	130	TGTCAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGA	189
Qy	144	CTCTCCCTGTGTGAGGCTCTGGATTTACTTTCTAGTGGCTACTGGATGCTGTGGGTCGGCCAG	203
Db	190	CTCTCCCTGTGCAGGCTCTGGAGTTCACTTTCAGTAAACGGCTGGATGAGCTGGGTCGGCCAG	249
Qy	204	TCTCCAGAGAAGGGCTGTGAGTGGGTGCTGAAATTAGATTGAAATCTGATAATTATGCA	263
Db	250	GCTCCAGGGAAGGGCTGGAGTGGGTTGGCCGTATTTAAAGCAAACTGATGTGGGACA	309
Qy	264	ACACATTATGCGGAGTCTGTGAAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAGT	323
Db	310	ACAGACTACGCTGACCCGTGAAGGCGAGATTCACCATCTCAAGAGATGATTCAAAAC	369
Qy	324	CGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGCTGGAGTTTATTACTGTAC	382
b	370	ACGTTGATCTGCAATCAACAGCTGAAACCGAGGACACGCGTATTACTGTAC	428

RESULT	15
AWS04516	
LOCUS	UI-HF-BN0-alj-c-03-0-Ut.rl NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION	linear mRNA 446 bp EST 02-MAR-2000
IMAGE:	3079684 5', mRNA sequence.
ACCESSION	AWS04516
VERSION	AWS04516.1 GI:7142183
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
1 (bases 1 to 446)	
NIH-MGC http://mgc.nci.nih.gov/.	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-re@mail.nih.gov	
Eco RI site shown at the beginning of the sequence.	
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.	
cDNA Library Preparation: M.B. Soares Lab	
cDNA Library Arrayed by: M.B. Soares Lab	
DNA Sequencing by: M.B. Soares Lab	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.biml.llnl.gov/bbrp/image/image.html Seq primer: M13 Forward.	

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FEATURES
  source
    Location/Qualifiers
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        /clone.lib="NIH_MGC_50"
        /tissue.type="lymph"
        /cell.type="germinal center B cells"
        /cell.type="MGC85"
        /cell_line="MGC85"
        /lab_host="DH10B (LT1)"
        /note="Vector: pVT3-Pac; Site_1: NotI; Site_2: Eco RI;
        Constructed from size fractionated cytoplasmic mRNA
        (3.5-4.4kb). Directionally cloned. Cells provided by
        Louis M. Staudt, Ph.D. Library preparation by Maria de
        Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      110 a      104 c      126 g      106 t
ORIGIN
  Query Match      50.0%;      Score 207.4;      DB 10;      Length 446;
  Best Local Similarity 75.8%;      Pred. No. 6.4e-39;
  Matches: 272;      Conservative      0;      Mismatches 81;      Indels 6;      Gaps 1

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Db 70 CTCACCATGGAGTTTGGGCTGAGCTGGATTTCCTTGGCTGCTATTTTAAAGGTGTCCAG 129
Qy 84 AGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAA 143
Db 130 TGTGAGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCTGGGGGTCCCTTAGA 189
Qy 144 CTCTCCTGTGTAGCCTCTGGATTACTTTCACTGGGCTACTGSGATGCTTGGGTCCGCCAG 203
Db 190 CTCTCCTGTGCAGCCTCTGGTTTCACTTTCAATAAGCCCTGGATGAACCTGGGTCCGCCAG 249
Qy 204 TCTCCAGAGAAGGGCTTGAGTGGTGTGCTGAATAGATTGAAATCTGNATATTATGCA 263
Db 250 GCTCCAGGGAAGGGCTGGAGTGGGTGGCCGTATTAAAGCAAACTGATGTTGGGACA 309
Qy 264 ACACATTATCGGAGTCTGTGAAAGGAAGTTCACCATCTCAAGAGATGATCCAAAAGT 323
Db 310 ACAGACTACGCTGCACCCGTGAAAGGCAGATTTCACCATCTCAAGAGATGATTCATAACC 369
Qy 324 CGTCTCTACCTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 370 ACGTCTTATCTGCAATGAACAGCCTGAAAACCGAAGACACACAGCCCGTGTATTACTGTAC 428

Search completed: April 26, 2003, 07:26:36
Job time : 557.077 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 83.4911 Seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716b-1
Perfect score: 415
Sequence: 1 aagctttacagtactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	100.0	415	21	Mouse anti-CD23 MA
2	310.4	74.8	453	22	Murine PSCA antio
3	310.4	74.8	453	24	Murine heavy chain
4	301.4	72.6	1774	20	Antibody ABX-CBL h
5	293.6	70.7	496	20	Coding strand for
6	293.6	70.7	497	11	Br-3 Heavy Chain V
7	293.6	70.7	497	18	Mab Br-3 heavy cha
8	289.4	69.7	480	15	Mab 4197X heavy ch
9	282.2	68.0	469	12	Sequence encoding

10	282.2	68.0	469	12	AAQ12016	Sequence encoding
11	272	65.5	357	19	AAV22331	Nucleic acid encod
12	271.6	65.4	856	22	AAC90472	Antibody 33F12 cat
13	269.8	65.0	1979	16	AAQ85386	Anti-cataract immu
14	269.4	64.9	403	15	AAQ62750	Murine BrE-3 immu
15	269.4	64.9	403	15	AAQ62750	Murine BrE-3 immu
16	268.6	64.7	498	12	AAQ11969	Sequence encoding
17	267.8	64.5	360	18	AAQ11969	Lead binding Mab 4
18	267.2	64.4	366	21	AAQ11969	2G3 hybridoma VH d
19	265.4	64.0	765	24	AAQ11969	P5-11 single chain
20	265.2	63.9	809	14	AAQ34841	Encodes VH region
21	265	63.9	350	20	AAQ31971	SM3 heavy chain va
22	263.6	63.5	899	22	AAC90471	Mouse antibody 38C
23	263	63.4	403	15	AAQ62791	Humanised murine B
24	262.4	63.2	768	24	AAQ62791	P5-2 single chain
25	262.4	63.2	1509	24	AAQ62791	3B10xP5-2 bispecif
26	260.6	62.8	5227	18	AAQ62791	Plasmid pTERMSC2H1
27	259	62.4	342	21	AAQ62791	113F1 hybridoma VH
28	256.6	61.8	357	18	AAQ62791	Lead binding Mab 7
29	256	61.7	357	18	AAQ62791	Humanised cA2 heav
30	256	61.7	357	19	AAQ62791	Coding sequence fo
31	256	61.7	357	20	AAQ62791	cDNA encoding heav
32	256	61.7	357	22	AAQ62791	Mouse heavy chain
33	256	61.7	357	22	AAQ62791	DNA encoding anti-
34	256	61.7	357	24	AAQ62791	Chimeric antibody,
35	255.4	61.5	1335	21	AAQ62791	Humanised anti-CD2
36	254.4	61.3	357	22	AAQ62791	Nucleotide sequenc
37	244.4	58.9	345	14	AAQ40046	BW 835 VH. Synthe
38	243.2	58.6	782	16	AAQ6755	Anti-dansyl single
39	238.4	57.4	387	17	AAQ74066	Monoclonal antibod
40	232.6	56.3	345	19	AAQ3191	Human H chain V re
41	232.6	56.0	741	22	AAQ8024	Murine anti-CA19-9
42	229.4	55.3	738	14	AAQ43293	Sequence encoding
43	229.4	55.3	738	15	AAQ66841	CC49 VL / 217 / 4-
44	229.4	55.3	738	20	AAQ4747	DNA encoding a pro
45	229.4	55.3	738	20	AAQ9764	Fusion polypeptide

ALIGNMENTS

RESULT 1
AA234745
ID AA234745 standard; cDNA; 415 BP.

AC AA234745;

DT 15-FEB-2000 (first entry)

DE Mouse anti-CD23 Mab C11 heavy chain variable region cDNA.

XX CD23; FCER1; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.

OS Mus musculus.

XX Key Location/Qualifiers
FH CDS 3..413
FT /*tag= a

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01434.

```

XX 09-MAY-1998; 98GB-0009839.
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX WPI; 2000-053101/04.
XX P-PSDB; AAY32260.
XX
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX Claim 16; Fig 1; 81pp; English.
XX
XX This DNA sequence encodes the heavy chain variable region (VH) of
XX murine anti-CD23 (FCER1I) monoclonal antibody C11. The invention
XX provides altered antibodies, such as chimeric or humanised
XX antibodies (see AAZ34747 and AAZ34748), which comprise sufficient of
XX the amino acid sequences of the C11 light and heavy chain
XX complementarity determining regions (see AAY32254-59) to render them
XX capable of binding to the CD23 type II molecule expressed on
XX haematopoietic cells. The antibodies are used to block soluble
XX CD23 formation in human therapy, for the treatment of arthritis,
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
XX asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
XX eczema, graft-versus-host disease, COPD, insulinitis, bronchitis,
XX (particularly chronic bronchitis) or diabetes (particularly type 1
XX diabetes), and B-cell malignancies (claimed). They are also useful
XX for studying interactions between CD23 and various ligands and
XX determining the binding agents.
XX
XX Sequence 415 BP; 111 A; 76 C; 110 G; 118 T; 0 other;
XX
XX Query Match 100.0%; Score 415; DB 21; Length 415;
XX Best Local Similarity 100.0%; Pred. No. 6.1e-115;
XX Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATTGGCTGATTTTGGCTGATTTTGA 60
XX Db 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATTGGCTGATTTTGGCTGATTTTGA 60
XX
XX QY 61 TTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
XX Db 61 TTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 120
XX
XX QY 121 TGCAACCTGGAGGATCCATGAACCTCTCCCTGTAGCTGTAGCTGTAGCTGTAGCTGTAGCTGT 180
XX Db 121 TGCAACCTGGAGGATCCATGAACCTCTCCCTGTAGCTGTAGCTGTAGCTGTAGCTGTAGCTGT 180
XX
XX QY 181 ACTGGATGCTTGGGTCGCCAGTCTCCAGAGAAGGGGCTTGAAGTGGTGTGCTGAATTA 240
XX Db 181 ACTGGATGCTTGGGTCGCCAGTCTCCAGAGAAGGGGCTTGAAGTGGTGTGCTGAATTA 240
XX
XX QY 241 GATTGAATCTGAATATGTAACACATATATCGGAGTCTGTGAAGGAAGTTCACCA 300
XX Db 241 GATTGAATCTGAATATGTAACACATATATCGGAGTCTGTGAAGGAAGTTCACCA 300
XX
XX QY 301 TCTCAAGAGATGATTCACAAAGTCGCTCTTACCTGCAATGAACAGCTTTAAGAGCTGAAG 360
XX Db 301 TCTCAAGAGATGATTCACAAAGTCGCTCTTACCTGCAATGAACAGCTTTAAGAGCTGAAG 360
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XX QY 361 ACAGTGGAGTTTATCTGTACAGATTTTATAGCTGGGGCCCAAGGACACTAGT 415
XX Db 361 ACAGTGGAGTTTATCTGTACAGATTTTATAGCTGGGGCCCAAGGACACTAGT 415
XX
XX RESULT -2
XX AAF27975
XX ID AAF27975 standard; DNA; 453 BP.

```

```

XX AAF27975;
XX AC
XX XX
XX DT 08-MAY-2001 (first entry)
XX
XX DE Murine PSCA antibody 2H9 H chain V region coding sequence.
XX DE
XX XX
XX KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
XX KW diagnosis; treatment; chromosome 8q24.2; ds.
XX OS
XX Mus sp.
XX PN WO200105427-A1.
XX PD
XX XX 25-JAN-2001.
XX
XX PF 20-JUL-2000; 2000WO-US19967.
XX XX
XX PR 20-JUL-1999; 99US-0359326.
XX PR 03-MAY-2000; 2000US-0564329.
XX XX
XX PA (REGC ) UNIV CALIFORNIA.
XX PA (UROC-) UROGENESYS.
XX
XX PI Reiter R, Witte O, Safran DC, Jakobovits A;
XX
XX DR WPI; 2001-159478/16.
XX DR P-PSDB; AAB35292.
XX
XX XX Antibodies binding to prostate stem cell antigen inhibit the growth of
XX PT cancer cells and are used to detect and treat prostate, pancreatic or
XX PT bladder cancers -
XX XX
XX PS Example 21; Fig 60; 229pp; English.
XX
XX CC The present invention describes a method of treating cancer associated
XX CC with prostate stem cell antigen (PSCA) by administering an antibody which
XX CC selectively binds to PSCA and inhibits the growth of the cancer cells.
XX CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
XX CC the human and murine PSCA protein and coding sequences, which can be used
XX CC not only in the treatment of, but also in detection and prognosis of
XX CC prostate cancer.
XX
XX SQ Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 other;
XX
XX Query Match 74.8%; Score 310.4; DB 22; Length 453;
XX Best Local Similarity 92.6%; Pred. No. 1.9e-83;
XX Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
XX
XX QY 35 CATGGATTTTGGCTGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 94
XX Db 6 CTTCGGGTGAGCTGGGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 65
XX
XX QY 95 GCTTCAGGAGTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACCTCTCTCTGTGT 154
XX Db 66 GCTTCAGGAGTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACCTCTCTCTGTGT 125
XX
XX QY 155 AGCCTCTGGATTTACTTTTCACTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAA 214
XX Db 126 AGCCTCTGGATTTACTTTTCACTGAATTTACTGATGCTTGGTCCGCCAGTCTCCAGAGAA 185
XX
XX QY 215 GGGCTTCAGTGGGTGCTGTAATTTAGATTTGAATTTGATTAATTTATGCAACACATTTATGC 274
XX Db 186 GGGCTTCAGTGGGTGCTGTAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 245
XX
XX QY 275 GGAGTCTGTGAAGGAAAGTTTCAACCTCAAGAGATGATTCCAAAGTCTCTCTCTACCT 334
XX Db 246 GGAGTCTGTGAAGGAAAGTTTCAACCTCAAGAGATGATTCCAAAGTCTCTCTCTACCT 305
XX
XX QY 335 GCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGGAGTTTATTTACTGTACAGAT 386
XX Db 306 GCAATGAACAACTTAAGAGCTGAAGAGCTGGAGTTTATTTACTGTACAGAT 357

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```

RESULT 3
ID ABK09984
XX ABK09984 standard; DNA; 453 BP.
AC ABK09984;
XX
DT 21-MAY-2002 (first entry)
XX
DE Mouse heavy chain variable domain region of PSCA antibody 2H9 gene.
XX
KW Mouse; prostate stem cell antigen; PSCA; gene; antibody; immunogen;
KW prostate cancer; bladder cancer; pancreatic cancer; immunconjugate;
KW PSCA-associated cancer; heavy chain variable domain region;
KW PSCA antigen; PSCA antibody 2H9; ds.
XX
OS Mus sp.
XX
FH Key
FH CDS
FH Location/Qualifiers
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FT /partial
FT /product= "Mouse PSCA antibody 2H9"
FT /note= "This sequence lacks both a start and stop codon"
FT misc_feature
FT 133..162
FT /*tag= b
FT /note= "Complementarity determining region 1 (CDR1)"
FT misc_feature
FT 205..261
FT /*tag= c
FT /note= "Complementarity determining region 2 (CDR2)"
FT misc_feature
FT 358..375
FT /*tag= d
FT /note= "Complementarity determining region 3 (CDR3)"
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US2001055751-A1.
XX
27-DEC-2001.
XX
03-MAY-2000; 2000US-0564329.
XX
10-MAR-1997; 97US-228816P.
XX
12-JAN-1998; 98US-071141P.
XX
13-FEB-1998; 98US-074675P.
XX
21-DEC-1998; 98US-113230P.
XX
17-FEB-1999; 99US-120536P.
XX
16-MAR-1999; 99US-124658P.
XX
10-MAR-1998; 98US-0038261.
XX
02-DEC-1998; 98US-0203939.
XX
17-FEB-1999; 99US-0251835.
XX
25-MAY-1999; 99US-0318503.
XX
20-JUL-1999; 99US-0359326.
XX
(REIT/) REITER R E.
XX
(WITT/) WITTE O N.
XX
(SAFF/) SAFFRAN D C.
XX
(JAKO/) JAKOBOVITS A.
XX
Reiter RE, Witte ON, Saffran DC, Jakobovits A;
XX
WPI: 2002-194864/25.
XX
P-PSDB; AAU76696.
XX
New antibodies specifically binding a novel prostate cell surface
XX
antigen, PSCA, useful as antitumour agents in treatment of prostate,
XX
bladder and pancreatic cancer and in prostate cancer diagnosis
XX
Example 21; Fig 60; 127pp; English.
XX
The present invention relates to new antibodies that specifically bind a
XX
novel prostate stem cell antigen (PSCA), which is widely over-expressed
XX
across all stages of prostate cancer. The antibodies of the invention
XX
are useful to kill tumour cells expressing PSCA and as PSCA expression is
XX
observed in prostate tumour cells and in other human cancers,

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CC particularly bladder and pancreatic carcinomas, the antibodies are
CC useful therapeutically to treat these diseases. In particular, monoclonal
CC antibodies can be administered to subjects suffering from PSCA-associated
CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic
CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong
CC the subject's life. The antibodies can be combined with a therapeutic
CC agent in immunoconjugates useful to treat subjects suffering from
CC malignant diseases, characterised by cells having PSCA antigen on the
CC cell surface e.g. cancers, by killing the cells. The antibodies and
CC immunoconjugates may also be included with a carrier in pharmaceutical
CC compositions useful to kill human cells expressing PSCA antigen on the
CC cell surface. The antibodies are also useful diagnostically to detect
CC cancers, especially prostate cancer, to isolate prostate cancer cells
CC e.g. to enable culture growth to evaluate candidate therapeutic
CC compounds, assist in identification of rare genes associated with
CC prostate cancer, and to isolate and purify PSCA and PSCA homologues.
CC The present nucleic acid sequence encodes the mouse heavy chain variable
CC domain region of the PSCA monoclonal antibody 2H9 of the invention.
XX
SQ Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 other;
Query Match 74.8%; Score 310.4; DB 24; Length 453;
Best Local Similarity 92.6%; Pred. No. 1.9e-83;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTGCGGCTGATTTTATTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGA 94
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 95 GCITGAGGAGTCTGGAGGAGGCTGGTGGCAACCTGGAGGATCCATGAACCTCTCCTGTGT 154
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 GCTTGGAGGAGTCTGGAGGAGGCTGGTGGCAACCTGGAGGATCCATGAACCTCTCCTGTGT 125
QY 155 AGCCTCTGGATTACTTTCAGTGGCTACTGGATGCTTGGTGGCGCCAGTCCAGAGAA 214
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 126 AGCCTCTGGATTACTTTCAGTGGCTACTGGATGCTTGGTGGCGCCAGTCCAGAGAA 185
QY 215 GGGCTTGGAGTGGTCTCTGAAATAGATTGAAATAGATTGAAATAGATTGAAATAGATTG 274
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 GGGCTTGGAGTGGTCTCTGAAATAGATTGAAATAGATTGAAATAGATTGAAATAGATTG 245
QY 275 GGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATTCGAAGTGGTCTCTACCT 334
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 246 GGAGTCTGTGAAGGGAGTTCACCATCTCAAGAGATGATTCGAAGTGGTCTCTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTGTATTACTGTACAGAT 386
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 306 GCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTGTATTACTGTACAGAT 357
RESULT 4
AAZ20419
ID AAZ20419 standard; cDNA; 1774 BP.
XX
AC AAZ20419;
XX
DT 19-NOV-1999 (first entry)
XX
DE Antibody ABX-CBL heavy chain coding sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS
FH Location/Qualifiers
FT 58..1770
FT /*tag= a
XX
FN W09945031-A2.
XX

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QY 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTATGCGAGTCTGTGAAAGGGA 291
 |||||
 Db 271 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTATGCGAGTCTGTGAAAGGGA 330
 |||||
 QY 292 AGTTCCACATCTCAAGAGATGATTCCTCAAAAGTCGTCTTACCTGCAATGAACAGCTTAA 351
 |||||
 Db 331 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGTCTTACCTGCAATGAACAGCTTAA 390
 |||||
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 |||||
 Db 391 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 422
 |||||

RESULT 6
 ID AAQ08605 standard; DNA; 497 BP.
 XX
 AC AAQ08605;
 XX
 DT 04-MAR-1993 (first entry)
 XX
 DE Br-3 Heavy Chain V Region (mouse).
 XX
 KW Monoclonal antibody; chimera; light; heavy; chain; constant;
 KW variable; antigen; diagnosis; cancer; tumour; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..495
 FT /*tag= a
 XX
 PN WO9002569-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 06-SEP-1989; 89WO-US03852.
 XX
 PR 06-SEP-1988; 88US-0240624.
 PR 08-SEP-1988; 88US-0241744.
 PR 13-SEP-1988; 88US-0243739.
 PR 04-OCT-1988; 88US-0253002.
 PR 19-JUN-1989; 89US-0367641.
 PR 21-JUL-1989; 89US-0382768.
 XX
 PA (ITGE-) INT GENETIC ENG INC.
 XX
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 XX
 DR WPI; 1990-115825/15.
 DR P-PSDB; AAR09423.
 XX
 PT Chimeric mouse-human antibodies - prepd. using genes coding for
 PT constant human region murine variable region, esp. to 3 tumour
 PT antigen
 XX
 PS Claim 13; Page 123 + Fig 15; 173pp; English.
 XX
 CC Shown is the nucleotide sequence from the end of the oligo-dC tail
 CC to the Jh3-Chl junction. The sequence is used in the prodn. of a
 CC chimeric antibody mol. comprising two light chains and two heavy chains,
 CC each having a constant region (human) and a variable region (murine)
 CC having specificity to an antigen bound by murine monoclonal antibody
 CC (MAB) Br-3. The chimeric antibodies can be used for any purpose for
 CC which the original murine MABs can be used, with the advantage that
 CC they are more compatible with the human body. They are esp. used for
 CC the diagnosis and treatment of cancer.
 XX
 SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 other;

Query Match 70.7%; Score 293.6; DB 11; Length 497;
 Best Local Similarity 92.8%; Pred. No. 2.3e-78;
 Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTTTATTGTTCTTTTAAAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 |||||
 Db 92 TATTCATAGTTTCTCTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 151
 |||||
 QY 112 GAGCTTGGTGCACACCTGGAGGATCCATGAACCTCTCTCTGTAGCTCTGGATTTACTTT 171
 |||||
 Db 152 GAGCTTGGTGCACACCTGGAGGATCCATGAACCTCTCTCTGTAGCTCTGGATTTACTTT 211
 |||||
 QY 172 TCAGTGGCTACTGATGCTTTGGGTCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 231
 |||||
 Db 212 TCAGTAACTATGTGATGAAGTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 271
 |||||
 QY 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTATGCGAGTCTGTGAAAGGGA 291
 |||||
 Db 272 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTATGCGAGTCTGTGAAAGGGA 331
 |||||
 QY 292 AGTTCCACATCTCAAGAGATGATTCCTCAAAAGTCGTCTTACCTGCAATGAACAGCTTAA 351
 |||||
 Db 332 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGTCTTACCTGCAATGAACAGCTTAA 391
 |||||
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 |||||
 Db 392 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 423
 |||||

RESULT 7
 AAT43437
 ID AAT43437 standard; CDNA; 497 BP.
 XX
 AC AAT43437;
 XX
 DT 12-FEB-1997 (first entry)
 XX
 DE MAb Br-3 heavy chain variable region CDNA.
 XX
 KW Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
 KW tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
 KW ovary carcinoma; cancer; diagnosis; therapy; heavy chain; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..497
 FT /*tag= a
 FT /product= Br-3 heavy chain V region
 XX
 EN US5576184-A.
 XX
 PD 19-NOV-1996.
 XX
 PF 06-SEP-1988; 88US-0240624.
 XX
 PR 06-MAY-1991; 91US-0659401.
 PR 06-SEP-1988; 88US-0240624.
 PR 08-SEP-1988; 88US-0241744.
 PR 13-SEP-1988; 88US-0243739.
 PR 04-OCT-1988; 88US-0253002.
 PR 19-JUN-1989; 89US-0367641.
 PR 21-JUL-1989; 89US-0382768.
 PR 27-DEC-1994; 94US-0364001.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
 XX
 DR WPI; 1997-011249/01.
 DR P-PSDB; AAW06212.
 XX
 PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
 PT used for the treatment and diagnosis of human cancers
 XX
 PS Example 3; Fig 15; 102pp; English.

XX A cDNA clone (AA043437) codes for the heavy chain variable region
 CC (AA06212) of mouse monoclonal antibody (Mab) Br-3, and extends from
 CC the end of the oligo-dC tail to the JH3-CH1 junction. It was obtd.
 CC from a Br-3 hybridoma cDNA library by screening with a mouse IgG1
 CC C region probe. Mab Br-3 (IgG1) binds to an antigen that is
 CC expressed on the surface of human lung, breast, colon and ovary
 CC carcinomas, but not on most normal adult tissues. Light chain and
 CC heavy chain variable region (see also AA043434-43) sequences can be
 CC used with human constant region sequences to express mouse-human
 CC chimeric antibodies in transformed host cells. The antibodies have
 CC specificity to human tumour antigens and can be used for the
 CC treatment and diagnosis of human cancer.

XX SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 other;

Query Match 70.7%; Score 293.6; DB 18; Length 497;
 Best Local Similarity 92.8%; Pred. No. 2.3e-78;
 Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTTTATTTGCTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 92 TATTCATAGTTTCTCTCTTAAAGGTGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 151
 QY 112 GAGGCTTGTCGAACCTGGAGGATCCAGAACTCTCTGCTAGCTCTGGATTTACTT 171
 DB 152 GAGGCTTGTCGAACCTGGAGGATCCAGAACTCTCTGCTAGCTCTGGATTTACTT 211
 QY 172 TCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTG 231
 DB 212 TCAGTAACTATTGGATGAAGTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTG 271
 QY 232 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 291
 DB 272 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 331
 QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351
 DB 332 GGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 391
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 DB 392 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 423

RESULT 8

ID AAQ85388 standard; cDNA; 480 BP.

AC AAQ85388;

XX 31-AUG-1995 (first entry)

DE Mab 4197X heavy chain variable region.

XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW pHb19; 4197X; monoclonal antibody; Mab; ds.

OS Synthetic.

XX Key Location/Qualifiers
 FT CDS 1..480
 FT /*tag= a

XX WO9503828-A.

XX 09-FEB-1995.

XX 15-JUL-1994; 94WO-US07919.

XX 02-AUG-1993; 93US-0101329.

XX

PA (HOUS-) HOUSTON BIOTECHNOLOGY INC.

XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;

XX WPI; 1995-082036/11.

DR P-PSDB; AAR70829.

XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.

XX Disclosure; Fig.2; 68pp; English.

XX An immunotoxin (given in AAR70827) comprises the heavy (VH) and light
 CC chain (VL) variable regions of anti-lens epithelium IgG3 Mab 4197X
 CC linked to ricin-A. cDNAs encoding the VL and VH regions of 4197X
 CC (AAQ85387-88, respectively) were obtained from hybridoma mRNA,
 CC amplified by PCR, and engineered for inclusion in the immunotoxin
 CC construct (AAQ85386).

XX SQ Sequence 480 BP; 131 A; 105 C; 115 G; 129 T; 0 other;

Query Match 69.7%; Score 289.4; DB 16; Length 480;
 Best Local Similarity 92.1%; Pred. No. 4.2e-77;
 Matches 305; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 52 TTTTATTTTATTTGCTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 79 TATTCATAGTTTGTGTTTAAAGGTGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 138
 QY 112 GAGGCTTGTCGAACCTGGAGGATCCATGAACTCTCTGCTAGCTCTGGATTTACTT 171
 DB 139 GAGGCTTGTCGAACCTGGAGGATCCATGAACTCTCTGCTAGCTCTGGATTTACTT 198
 QY 172 TCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTG 231
 DB 199 TCAGTAACTCTGGATGAAGTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTG 258
 QY 232 CTGAATTTAGATTGAATCTGATAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 291
 DB 259 CTGAATTTAGATTGAATCTGATAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 318
 QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTACCTGCAATGAACAGCTTAA 351
 DB 319 GGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTACCTGCAATGAACAGCTTAA 378
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
 DB 379 GAGCTGAAGACAGTGGAGTTTATTACTGTAC 409

RESULT 9

AAQ12060
 ID AAQ12060 standard; DNA; 469 BP.

XX AAQ12060;

XX 15-AUG-1991 (first entry)

DE Sequence encoding heavy chain variable region of murine
 DE IC11 immunoglobulin.

KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.

XX Mus musculus.

XX Key Location/Qualifiers
 FT CDS 67..468
 FT /*tag= a

XX /product= mouse Mab IC11 H-chain variable region
 PN WO9107493-A.


```
AAV22331
ID AAV22331 standard; cDNA to mRNA; 357 BP.
XX
XX AAV22331;
AC
XX
XX 06-JUL-1998 (first entry)
DT
XX
XX Nucleic acid encoding synthetic branched mucin type glycolipid.
DE
XX
XX Branched mucin type glycolipid; V region; heavy chain; antibody;
KW
XX cancer treatment; diagnosis; ss.
KW
XX
XX Synthetic.
OS
XX
XX JP10084963-A.
PN
XX
XX 07-APR-1998.
PD
XX
XX 12-SEP-1996; 96JP-0241725.
PF
XX
XX 12-SEP-1996; 96JP-0241725.
PR
XX
XX (TOYJ ) TOSOH CORP.
PA
XX
XX WPI; 1998-264850/24.
DR
XX P-PSDB; AAW46958.
DR
XX
XX Recognising branched mucin type synthetic glycolipid - using gene
PT fragment of an antibody, useful in cancer treatment and diagnosis
PT
XX
XX Claim 1; Pages 4-5; 6pp; Japanese.
PS
XX
XX The present sequence encodes a branched mucin type synthetic
CC glycolipid. A gene fragment encoding the V region of the heavy
CC chain of an antibody recognising the protein encoded by the present
CC sequence is claimed. The antibody gene fragment is useful for the
CC development of cancer treatments and diagnosing agents.
CC
XX
XX Sequence 357 BP; 99 A; 75 C; 93 G; 90 T; 0 other;
SQ
Query Match -65.5%; Score 272; DB 19; Length 357;
Best Local Similarity 94.9%; Pred. No. 6.4e-72;
Matches 281; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAACATC 146
DB 1 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAACATC 60
QY 147 TCCTGTGTAGCCCTCTGGATTACTTTTCACTGGCTACTGGATGCTTGGGTCCGCCAGTCT 206
DB 61 TCCTGTGTCCCTCTGGATTCACTTTCACTAGTACTAGTGAACCTGGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 266
DB 121 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 180
QY 267 CATATATCCGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCGAAAAGTCGT 326
DB 181 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCGAAAAGTCGT 240
QY 327 CTCTACCTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTTATTACTGTAC 382
DB 241 GTCTACTGCAATGAACACACITTAAGAGCTGAAGACACTGGCATTTATTACTGTAC 296
RESULT 12
ID AAC90472
AAC90472 standard; DNA; 856 BP.
XX
XX AAC90472;
AC
XX
XX 13-MAR-2001 (first entry)
DT
XX
```

```
DE
XX
XX Antibody 33F12 catalytic fragment nucleotide sequence.
KW
XX Antibody 33F12; ketone compound; antitumour; cytotoxic;
KW targeted drug delivery; ds.
XX
XX Unidentified.
OS
XX
XX WO200071556-A1.
PN
XX
XX 30-NOV-2000.
PD
XX
XX 24-MAY-2000; 2000WO-US14366.
PF
XX
XX 25-MAY-1999; 99US-0318661.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;
PI
XX
XX WPI; 2001-061339/07.
DR
XX P-PSDB; AAB50426.
DR
XX
XX New ketone compounds containing active agents useful as carriers for
PT e.g. antitumor agents, antibiotics or fluorescent molecules -
PT
XX
XX Disclosure; Fig 10; 45pp; English.
PS
XX
XX The present sequence may be used in the activation of new ketone prodrug
CC compounds containing active agents. The ketone derivatives are useful as
CC carriers for antitumour agents such as cytotoxic agents, where the
CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
CC epothilone or its therapeutically active analogue or an anthracycline
CC antibiotic such as doxorubicin or its therapeutically active analogue.
CC The ketone derivatives are useful for targeted drug delivery.
CC The inactive molecules in the ketone compounds are converted to
CC active molecules by retro-Michael reaction. The antibody has
CC bifunctional activity and specifically immunoreacts with cell surface
CC antigen of a target cell. The active ingredients can be mixed
CC effectively with excipients as per desired amount along with the
CC buffering agent to enhance the effectiveness and activity of the
CC compound.
XX
XX Sequence 856 BP; 195 A; 208 C; 228 G; 225 T; 0 other;
SQ
Query Match 65.4%; Score 271.6; DB 22; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.2e-71;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACATC 146
DB 450 GAGGTGATGCTGGTGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACATC 519
QY 147 TCCTGTGTAGCCTCTGGATTACTTTTCACTGGCTTCTGGATGCTTGGGTCCGCCAGTCT 206
DB 520 TCCTGTGTGGTGTCTGGATTAACTTCACTTCACTTGGATGCTTGGGTCCGCCAGTCT 579
QY 207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 266
DB 580 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATTATGCAACA 639
QY 267 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCGAAAAGTCGT 326
DB 640 CATTATGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCGAAAAGTCGT 699
QY 327 CTCTACCTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTTATTACTGTACAGAT 386
DB 700 CTCTACCTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTTATTACTGTACAGAT 759
QY 387 TTCATAGACT 396
DB 760 TATTTTACT 769
```



```
Db 143 TTAGTGATGCTGGATGGCTGGTCCGCCAGCTCTCCAGAGAAGGGGCTTGAGTGGGTG 202
Qy 232 CTGAATAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTCTGAAGCGGA 291
Db 203 CTGAATAGAAAACAAAGCAATAATCATGCAACATATATGATGAGTCTGTGAAGCGGA 262
Qy 292 AGTTCACCATCTCAAGAGATGATTCAAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCAAAAGTAGAGTGTACCTGCAAAATGATAAGCTTAA 322
Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCAAGCGGA 408
Db 323 GAGCTGAAGACAGTGGCCCTTTATTACTGTACTGGGAGTTTGTCTAACTGGGGCCAGCGGA 382
Qy 409 CACTAGT 415
Db 383 CTCTGGT 389

RESULT 15
AAQ62775
ID AAQ62775 standard; cDNA; 403 BP.
XX AC AAQ62775;
XX DT 24-JAN-1995 (first entry)
XX DE Murine BrE-3 immunoglobulin heavy chain variable domain cDNA.
XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;
XX KW chimeric antibody; human milk fat globule; BrE-3 VH-chain; ss.
XX OS Mus musculus.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..402
XX FT /tag= a
XX FT /note= "BrE-3 VH chain (no termination codon)"
XX FT mat_peptide
XX FT 58..402
XX FT /*tag= b
XX FT /product= heavy_chain_V-region
XX FN WO9411509-A.
XX PD 26-MAY-1994.
XX PE 16-NOV-1993; 93WO-US11445.
XX PR 16-NOV-1992; 92US-0977696.
XX PR 30-SEP-1993; 93US-0129930.
XX PR 08-OCT-1993; 93US-0134346.
XX PA (CANC-) CANCER RES FUND CONTRA COSTA.
XX PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
XX WP; 1994-183510/22.
XX New analogue peptide(s) comprising antibody variable regions -
XX used to develop prods. for use in the detection, diagnosis,
XX therapy and prevention of neoplasms
XX Example 11; Page 48; 109pp; English.
XX CC Primers J02, J03, J04, J014 and VHLBACK (AAQ62765-Q62769) were all
XX used to prepare cDNAs that encode the BrE-3 mouse Ig variable
XX domains. The amplified V-regions lacked constant regions so as to
XX produce less immunogenic polypeptides. A hybrid polypeptide was
XX prepared using human constant regions with the murine V regions.
XX The chimeric polypeptide retained the binding affinity of BrE-3
XX for human milk fat globule.
XX SQ Sequence 403 BP; 105 A; 73 C; 113 G; 112 T; 0 other;
```

```
Query Match 64.9%; Score 269.4; DB 15; Length 403;
Best Local Similarity 85.3%; Pred. No. 4.1e-71;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTATTTTGTCTTTTAAAAGGGTCCAGAGTGAAGCTTGAAGCTTGAAGCTTGAAG 111
Db 23 TCTTCATAGTTTCTCTTAAAGGTGTCACAGAGTGAAGCTTGAAGCTTGAAGCTTGAAG 82
Qy 112 GAGCTTGGTGCACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCCTCTGGATTTACTT 171
Db 83 GAGCTTGGTGCACCTGGAGGATCCATGAAACTCTCCTGTGTGTCTCTTCTGGATTTACTT 142
Qy 172 TCAGTGGCTACTGGATGCTCTTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATGCTGGATGGGACTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 202
Qy 232 CTGAATAGATTGAATCTGATAATTATGCAACACATATTGCGGAGTCTCTGAAGCGGA 291
Db 203 CTGAATAGAAAACAAAGCAATAATCATGCAACATATATGATGAGTCTCTGAAGCGGA 262
Qy 292 AGTTCACCATCTCAAGAGATGATTCAAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCAAAAGTAGAGTGTACCTGCAAAATGATAAGCTTAA 322
Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCAAGCGGA 408
Db 323 GAGCTGAAGACAGTGGCCCTTTATTACTGTACTGGGAGTTTGTCTAACTGGGGCCAGCGGA 382
Qy 409 CACTAGT 415
Db 383 CTCTGGT 389
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SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	310.4	74.8	453	10	US-09-564-329A-14
2	310.4	74.8	453	10	US-09-855-153-14
3	310.4	74.8	453	10	US-09-854-811-14
4	310.4	74.8	453	10	US-09-934-773-14
5	310.4	74.8	453	10	US-09-963-620-14
6	271.6	65.4	856	10	US-09-883-758-3
7	271.6	65.4	856	10	US-09-883-758-6
8	263.6	63.5	899	10	US-09-883-758-1
9	263.6	63.5	899	10	US-09-883-758-5
10	256	61.7	357	9	US-10-043-432-4
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13	256	61.7	357	10	US-09-766-535A-4
14	256	61.7	357	10	US-09-756-161A-4
15	256	61.7	357	12	US-10-010-229-4
16	256	61.7	357	12	US-10-043-450-4
17	256	61.7	357	12	US-10-044-534-4
18	204	49.2	443	10	US-09-840-459-96
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21	196.2	47.3	406	9	US-10-046-935-2168
22	196.2	47.3	406	9	US-09-878-178-2168
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24	194.8	46.9	424	10	US-09-730-857-28
25	193.2	46.6	364	7	US-08-779-784-14
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28	189	45.5	545	10	US-09-925-301-16
29	187.4	45.2	424	10	US-09-730-857-62
30	186.8	45.0	369	10	US-09-893-615-86
31	186.8	45.0	1437	9	US-10-124-905-7
32	186.8	45.0	1437	9	US-09-948-429B-7
33	185.8	44.8	1437	9	US-10-073-138-4
34	185.8	44.8	424	10	US-09-730-857-50
35	185.8	44.8	424	10	US-09-730-857-54
36	185.8	44.8	424	10	US-09-730-857-64
37	185.6	44.7	357	10	US-09-840-459-97
38	185.6	44.7	357	10	US-09-840-459-103
39	184.2	44.4	424	10	US-09-730-857-48
40	184.2	44.4	424	10	US-09-730-857-58
41	184.2	44.4	424	10	US-09-730-857-58
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43	184	44.3	690	9	US-10-105-891-73
44	183.6	44.2	630	9	US-10-040-244-14
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ALIGNMENTS

RESULT 1
US-09-564-329A-14
; Sequence 14, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-564-329A-14

Sequence 15, Appl
Sequence 2168, Ap
Sequence 2168, Ap
Sequence 2168, Ap
Sequence 28, Appl
Sequence 14, Appl
Sequence 3, Appl
Sequence 42, Appl
Sequence 16, Appl
Sequence 62, Appl
Sequence 86, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 4, Appl
Sequence 50, Appl
Sequence 54, Appl
Sequence 64, Appl
Sequence 97, Appl
Sequence 103, Appl
Sequence 48, Appl
Sequence 58, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 14, Appl
Sequence 14, Appl

Query Match	74.8%;	Score 310.4;	DB 10;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 1.4e-87;		
Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	35	CATGGAATTTGGCGTGATTTTTTTTATTGTCTTTTAAAGGGGTCCAGAGTGAAGTGAA	94	
Db	6	CTTGGGTTGAGCTGGGGTTTTTATTATTGTCTTTTAAAGGGGTCCGGAGTGAAGTCAG	65	
QY	95	GCTTGAGAGTCTGGAGGAGCGTTGGTGCACACCTGGAGGATCCATGAACATCTCCTGTGT	154	
Db	66	GCTTGAGAGTCTGGAGGAGCGTGGTGCACACCTGGAGGATCCATGAACATCTCCTGTGT	125	
QY	155	AGCCTCTGGATTTACTTTTCTAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAA	214	
Db	126	AGCCTCTGGATTTACTTTTCTAGTAATTAAGTGGATGCTGGTCCGCCAGTCTCCAGAGAA	185	
QY	215	GGGCGTTGAGTGGGTGCTGAAATTCAGATTCGAATCTCATATTAATATGCAACACATTATGC	274	
Db	186	GGGCGTTGAGTGGGTGCTGAAATTCGATTCGATTCGAAATTAATGCAACACATTATGC	245	
QY	275	GGAGTCTCTGAAAGGGGAAGTTACCATCTCAAGAGATGATTCCAAAAAGTCGTCTCTACCT	334	
Db	246	GGAGTCTGTGAAAGGGGAATTCACCATCTCAAGAGATGATTCGAGAGTCTGTCTCTACCT	305	
QY	335	GCAATGAACAGCTTATAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT	386	
Db	306	GCAATGAACACATTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT	357	

RESULT 2
 US-09-855-153-14
 ; Sequence 14, Application US/09855153
 ; Patent No. US20020102666A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PCSA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/855,153
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-09-855-153-14

US-09-855-153-14

•

[illegible]

RESULTS

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US-09-854-811-14
? Sequence 14, Application US/09854811
? Patent No. US20020119157A1
? GENERAL INFORMATION:
? APPLICANT: Reiter, Robert E.
? APPLICANT: Witte, Owen N.
? APPLICANT: Saffran, Douglas C.
? TITLE OF INVENTION: PSCA: PROSTATE STEM C
? FILE REFERENCE: 30435.54US14
? CURRENT APPLICATION NUMBER: US/09/854,811
? CURRENT FILING DATE: 2001-05-14
? PRIOR APPLICATION NUMBER: 09/564,329
? PRIOR FILING DATE: 2000-05-03
? PRIOR APPLICATION NUMBER: 09/359,326
? PRIOR FILING DATE: 1999-07-20
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 14
? LENGTH: 453
? TYPE: DNA
? ORGANISM: SCID Mice
US-09-854-811-14

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[illegible]

Query |

[illegible]

RESULT 4
 US-09-934-773-14
 ; Sequence 14, Application US/09934773
 ; Patent No. US2002013689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.34US14
 ; CURRENT APPLICATION NUMBER: US/09/934,773
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-09-934-773-14

QY 275 GGAGCTGTGAAGAGGGGAAGTTCACCATCTCAAGACAGATGATTTCCAAAGTCGTCTCTACCT 333
 Db 246 GGAGCTGTGAAGAGGGAAATTCACCACTCTCAAGAGATGATTCAGAAAGTCGTCTCTACCT 305
 QY 335 GCAAAATGAACAGCTTAAAGAGCTGAAGACAGTGGAGGTTTATTACTGTACAGAT 386
 Db 306 GCAAAATGAACAACTTAAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357
 RESULT 5
 US-09-963-620-14
 ; Sequence 14, Application US/09963620
 ; Patent No. US20020141941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435, 54US14
 ; CURRENT APPLICATION NUMBER: US/09/963,620
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-09-963-620-14

Query Match	74.8%;	Score 310.4;	DB 10;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 1.4e-87;		
Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	35	CATGGATTTGGGCTGATTTTTTTTATTCCTTTTAAAGGGGTCCAGAGTGAACGTGAA	94	
Db	6	CTTCGGGTTGAGTGGGTTTTTATTATTCCTTTTAAAGGGGTCCGGAGTGAAGTGAAG	65	
QY	95	GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAACACTCTCCTGTGT	154	
Db	66	GCTTGAGGAGTCTGGAGGAGGCTGGGTGCACCTGGAGATCCATGAACACTCTCCTGTGT	125	
QY	155	AGCCTCTGATTTACCTTCAGTGGCTACTGATGTCTTGGGTCCGCGACTCTCCAGAGAA	214	
Db	126	AGCCTCTGATTTACCTTCAGTAATTACTGGATGACTTGGGTCCGCGACTCTCCAGAGAA	185	
QY	215	GGGGCTTGAGTGGGGTTGCTCAAAATTAGATTGAAATCTGATAATTATGCAACACATTATGC	274	
Db	186	GGGGCTTGAGTGGGGTTGCTGAAATTCGATTGAGATCTGAAATATTATGCAACACATTATGC	245	

QY 275 GGAGTCTGTGAAGGGAAGTCCACCATCTCAAGAGATGATTCACAAAGTCGTCTTACT 334
|||||
Db 246 GGAGTCTGTGAAGGGAAGTCCACCATCTCAAGAGATGATTCACAAAGTCGTCTTACT 305
|||||
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGATTTATTACTGTACAGAT 386
|||||
Db 306 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGATTTATTACTGTACAGAT 357
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RESULT 6

US-09-883-758-3
; Sequence 3, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
; NAME/KEY: CDS
; LOCATION: (1)..(855)
US-09-883-758-3

Query Match 65.4%; Score 271.6; DB 10; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-75;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACTC 146
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Db 460 GAGGTGATGCTGGTGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACTC 519
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QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGGTCGCCAGTCT 206
|||||
Db 520 TCCTGTGTGGTCTGGATTTAACTTCAAGATTTCTGGATGCTTGGGTCGCCAGTCT 579
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QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGAATAGATTGAATCTGATAATTATGCAACA 266
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Db 580 CCAGAGAAGGGGCTTGAGTGGTGGTGAATAGATTGAATCTGATAATTATGCAACA 639
|||||
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
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Db 640 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 699
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QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGATTTATTACTGTACAGAT 386
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Db 700 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGATTTATTACTGTAAATC 759
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RESULT 7

US-09-883-758-6/c
; Sequence 6, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.

; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
US-09-883-758-6

Query Match 65.4%; Score 271.6; DB 10; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-75;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACTC 146
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Db 397 GAGGTGATGCTGGTGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAACTC 338
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QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGGTCGCCAGTCT 206
|||||
Db 337 TCCTGTGTGGTCTGTGGATTTAACTTTCAGTAGATTCTTGGTCCGCCAGTCT 278
|||||
QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGAATAGATTGAATCTGATAATTATGCAACA 266
|||||
Db 277 CCAGAGAAGGGGCTTGAGTGGTGGTGAATAGATTGAATCTGATAATTATGCAACA 218
|||||
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
|||||
Db 217 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 158
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QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGATTTATTACTGTACAGAT 386
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Db 157 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGATTTATTACTGTAAATC 98
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QY 387 TTCATAGACT 396
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Db 97 TATTTTACT 88
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RESULT 8

US-09-883-758-1
; Sequence 1, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

	Query Match	Best Local Similarity	63.5%;	Score 263.6;	DB 10;	Length 899;
	Matches 281;	Conservative	90.6%;	Pres. No. 9.9e-73;	Mismatches 29;	Indels 0; Gaps
Qy	87	GAGTCAACCTTGAGGAGCTTCGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAACCTC	146			
Db	434	GAGTGATGTTGGTGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGAACCATGAACCTC	375			
Qy	147	TCCTGTGTAGCCCTCGGATTTCATTTTCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCT	206			
Db	374	TCCTGTGAATTTCTGGATTAACTTTTCAGAAATTATGGATGCTTTGGTCCGCCAGTCT	315			
Qy	207	CCAGAGAAGGGCCCTTGAGTGGGTTGCTGAAATTTAGATTGAAATTCATATAATTTGCAACA	266			
Db	314	CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAGATCTGATAATTTATGCAACA	255			

	Query Match	63.5%	Score 263.6;	DB 10;	Length 899;
	Best Local Similarity	90.6%;	Pred. No. 9.9e-73;		
	Matches 281;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps
QY	-87	GAAGTGAACCTTGAGGAGCTCGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC	146		
DB	434	GAGGTGATGTTGGTGAGCTCGGAGGAGGCTTGGTGCACCTGGAGGAACCATGAACCTC			
QY	147	TCCTGTGTAGCCCTCGGATTTTACCTTCAGTGGCTACTGATGCTCTTGGTCCGCCAGTCT	206		
DB	374	TCCTGTGAAATTTCTCGGATTAACTTTACGAAATTTATGGATGCTCTGGTCCGCCAGTCT	315		
QY	207	CCAGAGAAGGGCCTTGAGTGGTTCCTCGAAATTTAGATTTGAAATCTCAATAATTGCCACA	266		
DB	314	CCAGAGAAGGGCCTTGAGTGGTTCCTCGAAATTTAGATTTGAGATCTGATAAATTATGCCACA	255		

Qy 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACCT 146
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db 1 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACCT 60

QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCCAGTCT 206
Db 61 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGGTTCGTAATAGATTGAAATCTGATATATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGGTTCGTAATAGATTGAAATCTGATATATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 240
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTTC 296

RESULT 13

US-09-766-535A-4
; Sequence 4, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09/766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-766-535A-4

Query Match 61.7%; Score 256; DB 10; Length 357;
Best Local Similarity 91.6%; Pred. No. 1.6e-70;

Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0:
QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCCAGTCT 206
Db 61 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGGTTCGTAATAGATTGAAATCTGATATATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGGTTCGTAATAGATTGAAATCTGATATATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGAGGAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 240
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTTC 296

RESULT 14

US-09-756-161A-4
; Sequence 4, Application US/09756161A
; Patent No. US2002013207A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09/756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-756-161A-4

Query Match 61.7%; Score 256; DB 10; Length 357;

Best Local Similarity 91.6%; Pred. No. 1.6e-70;
Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 87 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAGCTC 146
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAGCTC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTACGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTGTCTGGATTACTTTTACGTGGCTACTGGATGCTTGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGGTGGTCTGCTGAATAGATTGAATCTGATTAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGGTGGTCTGCTGAATAGATTGAATCTGATTAATATGCAACA 180
QY 267 CATTATCGGAGTCTGTGAAAGGGAGTTACCATCTCAAGAGATGATTCACAAAGTCT 326
Db 181 CATTATCGGAGTCTGTGAAAGGGAGTTACCATCTCAAGAGATGATTCACAAAGTCT 240
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTTC 296
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RESULT 15

US-10-010-229-4
; Sequence 4, Application US/10010229.

; Patent No. US20020114805A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/010,229
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)

Query Match

Best Local Similarity 61.7%; Score 256; DB 12; Length 357;
Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 87 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAGCTC 146
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAGCTC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTACGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTGTCTGGATTACTTTTACGTGGCTACTGGATGCTTGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGGTGGTCTGCTGAATAGATTGAATCTGATTAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGGTGGTCTGCTGAATAGATTGAATCTGATTAATATGCAACA 180
QY 267 CATTATCGGAGTCTGTGAAAGGGAGTTACCATCTCAAGAGATGATTCACAAAGTCT 326
Db 181 CATTATCGGAGTCTGTGAAAGGGAGTTACCATCTCAAGAGATGATTCACAAAGTCT 240
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QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAAATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTC 296
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Search completed: April 26, 2003, 09:24:04
Job time : 43.1085 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 17.1893 seconds
(without alignments)
7404.053 Million cell updates/sec

Title: US-09-674-716B-1
Perfect score: 415
Sequence: 1 aagctttacattactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271.6	65.4	856	4	US-09-318-661-3
2	271.6	65.4	856	4	US-09-318-661-6
3	269.4	64.9	403	1	US-07-977-696C-12
4	269.4	64.9	403	1	US-08-129-930B-12
5	269.4	64.9	403	4	US-08-976-288A-12
6	267.8	64.5	360	3	US-08-767-128-27
7	267.2	64.4	366	3	US-08-483-749A-1
8	263.6	63.5	899	4	US-09-318-661-1
9	263.6	63.5	899	4	US-09-318-661-5
10	263	63.4	403	1	US-07-977-696C-65
11	263	63.4	403	1	US-08-129-930B-65
12	263	63.4	403	4	US-08-976-288A-65
13	259	62.4	342	3	US-08-483-749A-9
14	256.6	61.8	357	3	US-08-767-128-25
15	256	61.7	357	1	US-08-192-102-4
16	256	61.7	357	1	US-08-324-799-4
17	256	61.7	357	2	US-08-192-861A-4
18	256	61.7	357	4	US-09-133-119-4
19	256	61.7	357	4	US-08-192-093A-4
20	244.4	58.9	345	1	US-08-488-661-2
21	244.4	58.9	345	1	US-08-466-272A-2
22	244.4	58.9	345	1	US-08-478-857-2
23	244.4	58.9	345	2	US-08-471-771-2
24	244.4	58.9	345	3	US-09-130-783-2
25	229.4	55.3	738	2	US-08-224-591-13
26	229.4	55.3	738	2	US-08-392-338A-22
27	229.4	55.3	738	2	US-08-926-789-13

28	229.4	55.3	738	3	US-09-166-750-22	Sequence 22, Appl
29	229.4	55.3	738	3	US-09-166-093-22	Sequence 22, Appl
30	229.4	55.3	738	3	US-09-172-019-22	Sequence 22, Appl
31	229.4	55.3	738	3	US-09-166-094-22	Sequence 13, Appl
32	229.4	55.3	738	5	PCT-US93-11138-13	Sequence 12, Appl
33	229.4	55.3	744	2	US-08-392-338A-12	Sequence 12, Appl
34	229.4	55.3	744	3	US-09-166-750-12	Sequence 12, Appl
35	229.4	55.3	744	3	US-09-166-093-12	Sequence 12, Appl
36	229.4	55.3	744	3	US-09-172-019-12	Sequence 12, Appl
37	229.4	55.3	744	3	US-09-166-094-12	Sequence 12, Appl
38	229.4	55.3	761	2	US-08-392-338A-14	Sequence 14, Appl
39	229.4	55.3	761	3	US-09-166-750-14	Sequence 14, Appl
40	229.4	55.3	761	3	US-09-166-093-14	Sequence 14, Appl
41	229.4	55.3	761	3	US-09-172-019-14	Sequence 14, Appl
42	229.4	55.3	761	3	US-09-166-094-14	Sequence 14, Appl
43	229.4	55.3	770	2	US-08-392-338A-16	Sequence 16, Appl
44	229.4	55.3	770	3	US-09-166-750-16	Sequence 16, Appl
45	229.4	55.3	770	3	US-09-166-093-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-318-661-3
; Sequence 3, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
; NAME/KEY: CDS
; LOCATION: (1)..(855)
US-09-318-661-3

Query Match 65.4%; Score 271.6; DB 4; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.7e-72;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY	87	GAAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGTCGCAACCTGGAGATCCATGAACATC	146
Db	460	GAGTGTAGCTGTGGAGCTGTGGAGGCTTGTCGCAACCTGGAGATCCATGAACATC	519
QY	147	TCCTGTAGCTGTGGATTTACTTTTCAGTGGCTTCTGGGTCGCCAGTCT	206
Db	520	TCCGTGTGGTGTGGATTAACCTTCAGTAGATCTGGGATCTTGGGTCGCCAGTCT	579
QY	207	CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATATTTATGAACA	266
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QY	267	CATTATCGGAGCTGTGTAAGGGAAGTTTCAACATCTCAAGATGATTTCCAAAGTCGT	326
Db	640	CATTATCGGAGCTGTGTAAGGGAAGTTTCAACATCTCAAGATGATTTCCAAAGTCGT	699
QY	327	CTCTACCTGCAATGAACAGCTTAAGAGCTCAACAGATGAGTTTATTACTGTACAGAT	386
Db	700	CTCTACCTGCAATGAACAGCTTAAGAGCTCAACAGATGAGTTTATTACTGTAAATC	759

QY 387 TTCATAGACT 396
| | | | |
Db 760 TATTTTACT 769

RESULT 2

US-09-318-661-6/c
; Sequence 6, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
US-09-318-661-6

Query Match 65.4%; Score 271.6; DB 4; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.7e-72;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGGAGGCTCTGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 146
| | | | |
Db 397 GAGGTGATGCTGGTGGAGCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACCTC 338
QY 147 TCCTGTGTAGCTCTGATTTACTTTTCAGTGGCTTCTGAGTGTCTGGGGTCCGCCAGTCT 206
| | | | |
Db 337 TCCTGTGTGGTGTCTGGATTAACTTCAGTAGATTCTGAGTGTCTGGGGTCCGCCAGTCT 278
QY 207 CCAGAGAAGGGCTTGGTGGTGTCTGAAATTAGATTGAAATCTGATTAATTATGAACA 266
| | | | |
Db 277 CCAGAGAAGGGCTTGGTGGTGTCTGAAATTAGATTGAAATCTGATTAATTATGAACA 218
QY 267 CATTTATGCGGAGTCTGTGAAGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 326
| | | | |
Db 217 CATTTATGCGGAGTCTGTGAAGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 158
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTATTTACTCTACAGAT 386
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Db 157 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTATTTACTGTAAATC 98
QY 387 TTCATAGACT 396
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Db 97 TATTTTACT 88

RESULT 3

US-07-977-696C-12
; Sequence 12, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-977-696C-12

Query Match 64.9%; Score 269.4; DB 1; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 52 TTTTCTTATTCTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
| | | | |
Db 23 TCTTCATAGTCTTTCTTTAAAGGTGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 82
QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTACTT 171
| | | | |
Db 83 GAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTACTT 142
QY 172 TCAGTGGCTTACTGTGATGCTTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGTGG 231
| | | | |
Db 143 TTAGTGATGCTTGGTGGAGTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGTGG 202
QY 232 CTGAATTTAGATTGAATCTGATTAATTATGCAACACATTTATGCGGAGTCTGTGAAGGGA 291
| | | | |
Db 203 CTGAATTTAGAACCAAGCCCAATTAATCATGCAACATATTATGATGAGTCTGTGAAGGGA 262
QY 292 AGTTCAACATCTCAAGAGATGATTCCAAAGTCGCTCTACCTGCAAAATGAACAGCTTAA 351
| | | | |
Db 263 GGTTCACCATCTCAAGAGATGATTCCAAAGTAGAGTACCTGCAAAATGAATAGACTTAA 322
QY 352 GAGCTGAAGACAGTGGAGTCTTTATTACTGTAC---AGATTTATAGACTGGGCCAAGGGA 408
| | | | |
Db 323 GAGCTGAAGACAGTGGCCTTTATTACTGTCTGCGGAGTCTTGTCTAACTGGGCCAAGGGA 382
QY 409 CACTAGT 415
| | | | |
Db 383 CTCTGGT 389

RESULT 4

US-08-129-930B-12
; Sequence 12, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-129-930B-12

Query Match 64.9%; Score 269.4; DB 1; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTCTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 111
Db 23 TCTCATAGTCTTTCTCTTAAAGGTGCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 82
Qy 112 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
Db 83 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142
Qy 172 TCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATCGCTGGATGGAGTGGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 202
Qy 232 CTGAATATTAGATTGAATCTGTAATATTGCAACACATTATCGGAGTCTGTGAAGGGA 291
Db 203 CTGAATATTAGAACCAAGCCCAATATCATGCAACATATTATGATGATGCTGTGAAGGGA 262
Qy 292 AGTTCCACCATCTCAAGAGATGATTCACAAAGTCGCTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCACAAAGTAGAGTGTACCTGCAAAATGATAAGCTTAA 322
Qy 352 GAGCTGAACAGCTGGAGTTTATTACTGTAC--AGATTTCATAGACTGGGCCCAAGGGA 408
Db 323 GAGCTGAACAGACTGGCCCTTATTACTGTACTGGGAGGTTTGTCTAACTGGGCCCAAGGGA 382
Qy 409 CACTAGT 415
Db 383 CTCGTGT 389

RESULT 5
US-08-976-288A-12
Sequence 12, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-976-288A-12

Query Match 64.9%; Score 269.4; DB 4; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTCTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 111
Db 23 TCTCATAGTCTTTCTCTTAAAGGTGCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 82
Qy 112 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
Db 83 GAGGCTTGTCGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142
Qy 172 TCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATCGCTGGATGGAGTGGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 202
Qy 232 CTGAATATTAGATTGAATCTGTAATATTGCAACACATTATGCGGAGTCTGTGAAGGGA 291
Db 203 CTGAATATTAGAACCAAGCCCAATATCATGCAACATATTATGATGATGCTGTGAAGGGA 262

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QY 292 AGTTCCACATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAATGAACAGCTTAA 351
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Db 263 GGTTCACCATCTCAGAGATGATTCACAAAGTAGAGTCTACCTGCAATGAAGCTTAA 322
      |||||||
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTTCATAGACTGGGGCCCAAGGGA 408
      |||||||
Db 323 GAGCTGAAGACACTGGCCTTTATTACTGTACTGGGAGTTTGCTAACTGGGGCCAGGGA 382
      |||||||
QY 409 CACTAGT 415
      ||||
Db 383 CTCTGGT 389

RESULT 6
US-08-767-128-27
; Sequence 27, Application US/08767128
; Patent No. 611079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USE1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
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; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...360
; OTHER INFORMATION:
US-08-767-128-27

Query Match 64.5%; Score 267.8; DB 3; Length 360;
Best Local Similarity 92.7%; Pred. No. 1.8e-71;
Matches 281; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCCAACTGGAGGATCCATGAACCTC 146
      |||||||
Db 1 GAAGTGAAGACTGAGGAGTCTGGAGGAGGCTTGGTCCAACTGGAGGATCCATGAACCTC 60

QY 147 TCGTGTAGCCTCTGGATTACTTTTCAGTGGCTACTTGGATGCTCTTGGTCCGCCAGTCT 206
      |||||||
Db 61 TCGTGTGTTGCCCTCTGGATTCACTTTTCAGTAACTACTACTGATGAAGTGGTCCGCCAGTCT 120

QY 207 CCAGAGAAGGGGCTTGAGTGGGTTCTGCTGAATTAGATTCAAACTCTGATAATTATGCAACA 266
      |||||||
Db 121 CCAGAGAAGGGGCTTGAGTGGGTTCTGCTGAATTAGATTCAAACTCTGATAATTATGCAACA 180

QY 267 CATTATGCGGAGTCTGTGAAAGGGAAGTTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326
      |||||||
Db 181 CATTATGCGGAGTCTGTGAAAGGGAAGTTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 240

QY 327 CTCCTACTGCAATGAACAGACTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
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Db 241 GTCCTACTGCAATGAACAACTTAAAGAGCTGAAGACAGTGGCAATTTATTACTGTACCGGT 300

QY 387 TTC 389
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Db 301 TAC 303

RESULT 7
US-08-483-749A-1
; Sequence 1, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..366
US-08-483-749A-1

Query Match      64.4%; Score 267.2; DB 3; Length 366;
Best Local Similarity 93.9%; Pred. No. 2.7e-71;
Matches 278; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 146
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 60
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTCTTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTGCTCTGGATTCACCTTTTCAGTAACTACTGGATGAACCTGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATGAAATCTGAAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATGAAATCTGAAATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATCCAAAGTAGT 240
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAACTGAACAACTTAAGAGCTGAAGACAGTGGCATTTATTACTGTGC 296

RESULT 8
US-09-318-661-1
; Sequence 1, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-318-661-1

Query Match      63.5%; Score 263.6; DB 4; Length 899;
Best Local Similarity 90.6%; Pred. No. 4.5e-70;
Matches 281; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTTGAGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 146
Db 434 GAGGTGATGTTGGTGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 375
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTCTTGGTCCGCCAGTCT 206
Db 374 TCCTGTGAAATTTCTGGATTAACCTTCAGAAATTTATTGGATGCTCTTGGTCCGCCAGTCT 315
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGCTGAAATTAGATTGAATTCGAAATTCGAAATTCGAAAC 266
Db 314 CCAGAGAAGGGCTTGAGTGGTTCGCTGAAATTAGATTGAATTCGAAATTCGAAATTCGAAAC 255
QY 267 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATTCGAAAGAGTCTGT 326
Db 254 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATTCGAAAGAGTCTGT 195
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 386
Db 194 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 135
QY 387 TTCATAGACT 396
Db 134 TATTTTACT 125

RESULT 10
US-07-977-696C-65
; Sequence 65, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
```

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Db 646 CATTATCGGAGCTCTGTAAGGGAAGTTCCACCATCTCAAGAGATGATTCGAAAGAGTCGT 705
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 386
Db 706 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 765
QY 387 TTCATAGACT 396
Db 766 TATTTTACT 775
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RESULT 9
US-09-318-661-5/c
; Sequence 5, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-318-661-5
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Query Match      63.5%; Score 263.6; DB 4; Length 899;
Best Local Similarity 90.6%; Pred. No. 4.5e-70;
Matches 281; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTTGAGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 146
Db 434 GAGGTGATGTTGGTGGAGCTCTGGAGGAGGCTTGGTCCAACTCGGAGGATCCATGAACCTC 375
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTCTTGGTCCGCCAGTCT 206
Db 374 TCCTGTGAAATTTCTGGATTAACCTTCAGAAATTTATTGGATGCTCTTGGTCCGCCAGTCT 315
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGCTGAAATTAGATTGAATTCGAAATTCGAAATTCGAAAC 266
Db 314 CCAGAGAAGGGCTTGAGTGGTTCGCTGAAATTAGATTGAATTCGAAATTCGAAATTCGAAAC 255
QY 267 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATTCGAAAGAGTCTGT 326
Db 254 CATTATCGGAGCTCTGTAAGGGAAGCTTCACCATCTCAAGAGATGATTCGAAAGAGTCTGT 195
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 386
Db 194 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTACAGAT 135
QY 387 TTCATAGACT 396
Db 134 TATTTTACT 125
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RESULT 10
US-07-977-696C-65
; Sequence 65, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
```

;; TITLE OF INVENTION: and Therapeutic Methods.
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;; STREET: 444 South Flower Street, Suite 2000
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/977,696C
;; FILING DATE: 11-16-92
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amzel Ph.D., Viviana
;; REGISTRATION NUMBER: 30,930
;; REFERENCE/DOCKET NUMBER: P66.38227
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 748-6868
;; TELEFAX: (510) 748-6868
;; TELEX: n.a.
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 403 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-977-696C-65

Query Match 63.4%; Score 263; DB 1; Length 403;
Best Local Similarity 84.2%; Pred. No. 5.2e-70;
Matches 309; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

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QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTCTGAGGAGTCTGGAG 111
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DB 23 TCTTCATAGTTTTTCTCTTAAAGGTGTCCAGAGTGAAGTCTGTTGGAGTCTGGAG 82

QY 112 GAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
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DB 83 GAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142

QY 172 TCAGTGGCTACTGATGCTTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTTG 231
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DB 143 TTAGTGATGCTGTGATGAGTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTTG 202

QY 232 CTGAATTTAGATTGAATCTGATAATATGCAACACATATATGCGGAGTCTGTGAAAGGGA 291
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DB 203 CTGAATTTAGAAACAAGCCCAATATCATGCAACATATATGATGAGTCTGTGAAAGGGA 262

QY 292 AGTTTACCATCTCAAGAGATGTTCCAAAAGTCTCTACCTGCAATGAACAGCTTAA 351
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DB 263 GGTTCACCATCTCAAGAGATGTTCCAAAAGTCTCTACCTGCAATGAATAGCTTAA 322

QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCAAGGGA 408
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DB 323 GAGCTGAAGACACTGCCCTTTATTACTGTACTGGGGAGTTTGTACTGGGCCAAGGGA 382

QY 409 CACTAGT 415
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DB 383 CTCGTGT 389
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RESULT 11

US-08-129-930B-65

; Sequence 65, Application US/08129930B

; Patent No: 5804187

; GENERAL INFORMATION:

;; APPLICANT: do Couto Dr., Fernando J.R.
;; APPLICANT: Ceriani Dr., Roberto L.
;; APPLICANT: Peterson Dr., Jerry A.
;; APPLICANT: Padlan Dr., Eduardo A.
;; TITLE OF INVENTION: Analogue Peptides With Broad
;; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
;; TITLE OF INVENTION: Diagnostic Vaccination and
;; TITLE OF INVENTION: Therapeutic Methods
;; NUMBER OF SEQUENCES: 96
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: V. AMZEL & ASSOC.
;; STREET: 2055 No. 5804187th Broadway, Suite 201
;; CITY: Walnut Creek
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94596
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/129,930B
;; FILING DATE: September 30, 1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amzel Ph.D., Viviana
;; REGISTRATION NUMBER: 30,930
;; REFERENCE/DOCKET NUMBER: CRFCC-008A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 521-1333
;; TELEFAX: (510) 521-3541
;; TELEX: n.a.
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 403 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-129-930B-65

Query Match 63.4%; Score 263; DB 1; Length 403;

Best Local Similarity 84.2%; Pred. No. 5.2e-70;

Matches 309; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

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QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTCTGAGGAGTCTGGAG 111
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DB 23 TCTTCATAGTTTTTCTCTTAAAGGTGTCCAGAGTGAAGTCTGTTGGAGTCTGGAG 82

QY 112 GAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 GAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142

QY 172 TCAGTGGCTACTGATGCTTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTTG 231
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DB 143 TTAGTGATGCTGTGATGAGTGGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTTG 202

QY 232 CTGAATTTAGATTGAATCTGATAATATGCAACACATATATGCGGAGTCTGTGAAAGGGA 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 CTGAATTTAGAAACAAGCCCAATATCATGCAACATATATGATGAGTCTGTGAAAGGGA 262

QY 292 AGTTTACCATCTCAAGAGATGTTCCAAAAGTCTCTACCTGCAATGAACAGCTTAA 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 GGTTCACCATCTCAAGAGATGTTCCAAAAGTCTCTACCTGCAATGAATAGCTTAA 322

QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCAAGGGA 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 GAGCTGAAGACACTGCCCTTTATTACTGTACTGGGGAGTTTGTACTGGGCCAAGGGA 382

QY 409 CACTAGT 415
   ||| |||
DB 383 CTCGTGT 389
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; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,852
; FILING DATE: 11-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,606
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/670,827
; FILING DATE: 18-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: NYU93-01M3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..357
; US-08-192-102-4

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Query Match      61.7%; Score 256; DB 1; Length 357;
Best Local Similarity 91.6%; Pred. No. 6.3e-68;
Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 87 GAAGTGAAGCTTGAGGAGCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAACTC 146
Db 1 GAAGTGAAGCTTGAGGAGCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAACTC 60

Qy 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTCTGATGATGCTTGGGTCGCCCACTCT 206
Db 61 TCCTGTGTGTCTGCTGCTGATTCATTTTCAGTAACCACTGGATGAACCTGGGTCGCCCACTCT 120

Qy 207 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAATCTGATTAATTATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTAGATTGAATCTGATTAATTATGCAACA 180

Qy 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 181 CATTATGCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 240

Qy 327 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 CTCCTACCTGCAAAATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTC 296

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Job time : 20.1893 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 872.104 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716b-2
Perfect score: 437
Sequence: 1 aagctttacagtactacgc.....agttgggaataaaacgtacg 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
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- 35: em.htg.rod.*
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- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
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	4	371.6	85.0	458	10	MUSIGKCNF	M19909 Mouse Ig re
	5	333.4	76.3	1400	10	MUSIGKAH	J00553 Mouse Ig ka
	6	326.8	74.8	339	10	MMU29425	U29425 Mus musculu
	7	317.2	72.6	339	6	AR072863	AR072863 Sequence
8	317.2	72.6	339	6	AR166313	AR166313 Sequence	
9	317.2	72.6	368	6	AR072861	AR072861 Sequence	
10	317.2	72.6	368	6	AR166317	AR166317 Sequence	
11	316	72.3	420	6	AR166319	AR166319 Sequence	
12	309.2	70.8	368	6	AR072865	AR072865 Sequence	
13	309.2	70.8	368	6	AR166315	AR166315 Sequence	
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17	308	70.5	1060	10	MUSIGKVT1	K02415 Mouse Ig ge	
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34	275.2	63.0	993	10	AF466768	AF466768 Mus muscu	
35	262.2	60.0	339	10	AF087033	AF087033 Mus muscu	
36	257.2	58.9	348	6	AX010614	AX010614 Sequence	
C	37	257.2	58.9	348	6	AX010645	AX010645 Sequence
38	256.2	58.6	16329	2	AC118484	AC118484 Rattus no	
39	255.6	58.5	720	6	E35205	E35205 Human monoc	
40	254.6	58.3	720	6	E35208	E35208 Human monoc	
41	253.4	58.0	972	9	BC030814	BC030814 Homo sapi	
42	253	57.9	720	6	E35207	E35207 Human monoc	
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45	252.2	57.7	410	9	HS1GKLV46	X72467 H.sapiens m	

ALIGNMENTS

RESULT 1	AX010601	AX010601	Sequence 2 from Patent WO9958679.	437 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX010601	Sequence 2 from Patent WO9958679.					
DEFINITION	AX010601	Sequence 2 from Patent WO9958679.					
ACCESSION	AX010601	Sequence 2 from Patent WO9958679.					
VERSION	AX010601.1	GI:9997413					
KEYWORDS	house mouse.						
SOURCE	Mus musculus						
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
REFERENCE	1 (bases 1 to 437)						
AUTHORS	Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.						
TITLE	Antibodies to cd23, derivatives thereof, and their therapeutic uses						
JOURNAL	Patent: WO 9958679-A 2 18-NOV-1999;						

BONNEFOY JEAN YVES MARCEL PAUL (FR); CROME SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source Location/Qualifiers 1. .437 /organism="Mus musculus" /db_xref="taxon:10090" CDS <3. .>437 /note="unnamed protein product" /codon_start=1 /protein_id="CAC07527.1" /db_xref="GI:9997414" /translation="ALQLSTDLTWRESVQFLGLVFWISGVSDIIVITDELSPV TSGSVSISRSKSLLYKDKYILNWFQRCQSPOLLNMYLMSTRASGVDRFSGSG SGDTFLISRVKAEDEVVYICQOLVPEYFFTSGSGTKLEIKRT"

BASE COUNT 108 a 93 c 114 g 122 t

Query Match 100.0%; Score 437; DB 6; Length 437; Best Local Similarity 100.0%; Pred. No. 9.4e-133; Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTTCTGTTCTGG 60 DB 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTTCTGTTCTGG 60 QY 61 GGGTGTATTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC 120 DB 61 GGGTGTATTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC 120 QY 121 TCCTCAATCCTGCTACTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCGTAGTAAGAGTC 180 DB 121 TCCTCAATCCTGCTACTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCGTAGTAAGAGTC 180 QY 181 TCCTGTATAAGGATGGGAAGACATCTTGAATTCGTTCTGCAGAGACAGGACAAATCTC 240 DB 181 TCCTGTATAAGGATGGGAAGACATCTTGAATTCGTTCTGCAGAGACAGGACAAATCTC 240 QY 241 CTCAGTCTCTGATGATTTGATGTCACCCGTCATCAGGAGTCACAGCGGTTTGTAGTG 300 DB 241 CTCAGTCTCTGATGATTTGATGTCACCCGTCATCAGGAGTCACAGCGGTTTGTAGTG 300 QY 301 GCAGTGGGTGAGGACAGATTTCCACCTGGAAATCAGTAGAGTCGAGGCTGAGGATGTGG 360 DB 301 GCAGTGGGTGAGGACAGATTTCCACCTGGAAATCAGTAGAGTCGAGGCTGAGGATGTGG 360 QY 361 GTGTGTATTACTGTCAACAACCTGTAGAGTATCCATTCAGGTCGGGTCGGGACAAAGT 420 DB 361 GTGTGTATTACTGTCAACAACCTGTAGAGTATCCATTCAGGTCGGGTCGGGACAAAGT 420 QY 421 TGGAAATAAACGTCAG 437 DB 421 TGGAAATAAACGTCAG 437

RESULT 2 AX010644/c LOCUS Sequence 47 from Patent WO958679. DNA linear PAT 06-SEP-2000 AX010644 AX010644 AX010644.1 GI:9997453

REFERENCE AUTHORS Bonnefoy,J.Y., Crome,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J. Antibodies to cd23, derivatives thereof, and their therapeutic uses Patent: WO 958679-A 47 18-NOV-1999; BONNEFOY JEAN YVES MARCEL PAUL (FR); CROME SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source Location/Qualifiers 1. .437 /organism="Mus musculus" /db_xref="taxon:10090"

BASE COUNT 122 a 114 c 93 g 108 t

Query Match 100.0%; Score 437; DB 6; Length 437; Best Local Similarity 100.0%; Pred. No. 9.4e-133; Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTTCTGTTCTGG 60 DB 437 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTTCTGTTCTGG 378 QY 61 GGGTGTATTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC 120 DB 377 GGGTGTATTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAAC 318 QY 121 TCCTCAATCCTGCTACTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCGTAGTAAGAGTC 180 DB 317 TCCTCAATCCTGCTACTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCGTAGTAAGAGTC 258 QY 181 TCCTGTATAAGGATGGGAAGACATCTTGAATTCGTTCTGCAGAGACAGGACAAATCTC 240 DB 257 TCCTGTATAAGGATGGGAAGACATCTTGAATTCGTTCTGCAGAGACAGGACAAATCTC 198 QY 241 CTCAGTCTCTGATGATTTGATGTCACCCGTCATCAGGAGTCCTCAGACCGGTTTGTAGTG 300 DB 197 CTCAGTCTCTGATGATTTGATGTCACCCGTCATCAGGAGTCCTCAGACCGGTTTGTAGTG 138 QY 301 GCAGTGGGTGAGGACAGATTTCCACCTGGAAATCAGTAGAGTCGAGGCTGAGGATGTGG 360 DB 137 GCAGTGGGTGAGGACAGATTTCCACCTGGAAATCAGTAGAGTCGAGGCTGAGGATGTGG 78 QY 361 GTGTGTATTACTGTCAACAACCTGTAGAGTATCCATTCAGGTCGGGTCGGGACAAAGT 420 DB 77 GTGTGTATTACTGTCAACAACCTGTAGAGTATCCATTCAGGTCGGGTCGGGACAAAGT 18 QY 421 TGGAAATAAACGTCAG 437 DB 17 TGGAAATAAACGTCAG 1

RESULT 3 MUSIGKNCG LOCUS Mouse Ig rearranged kappa-chain mRNA, clone AN06K. ROD 26-MAR-1994 DEFINITION M19910 J03832 ACCESSION M19910.1 GI:197027 VERSION C-region: immunoglobulin light chain; immunoglobulin-kappa; KEYWORDS PROCESSED GENE. Mus musculus

SOURCE ORGANISM Mus musculus Mouse (BALB/c) mature B cell, cDNA to mRNA, clone AN06K. REFERENCE AUTHORS Rule,G.S. JOURNAL Unpublished (1988) REFERENCE AUTHORS Leach,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M. JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988) MEDLINE 88234486 PUBLISHED 3375235 COMMENT Draft entry and computer-readable sequence [2] kindly submitted by G.Rule, 20-JUL-1988. Location/Qualifiers 1. .431 /organism="Mus musculus" /strain="BALB/c" /sub_species="domesticus"

FEATURES source Location/Qualifiers 1. .431 /organism="Mus musculus" /strain="BALB/c" /sub_species="domesticus"

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VKAEDVGYYCQQLVEFLTFGAGTKLELR"
32..91
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mat_peptide
92..>431
/product="immunoglobulin kappa-chain"
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Best Local Similarity 94.4%; Pred. No. 1.1e-111;
Matches 387; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCAGTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGGATCTCT 83
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 20 CAAGTTCTCAGATGAGTCTCTTCAGTTCCTGGGGTGCCTATGTTCTGGATCTCT 79
QY 84 GAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGTCACCTCTGGA 143
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 80 GGAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGTCACCTCTGGA 139
QY 144 GAATCAGTTTCCATCTCTCGAGTCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 203
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 140 GAATCAGTTTCCATCTCTCGAGTCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 199
QY 204 TACTTGAATGGTTTCTCAGAGACCAGGACAATCTCTCAGCTCCTGATATTGATG 263
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 200 TACTTGAATGGTTTCTCAGAGACCAGGACAATCTCTCAGCTCCTGATATTGATG 259
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTC 323
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 260 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTC 319
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 383
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 320 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 379
QY 384 GTAGAGTATCCATTACGTTCCGTCGGGGACAAAGTTGGAATAAAACG 433
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 380 GTAGAGTTTCGGCTCACGTTCCGTCGGGACCAAGCTGGAGCTGAAACG 429

RESULT 4
MUSIGKCNF 458 bp mRNA linear ROD 26-MAR-1994
LOCUS Mouse Ig rearranged kappa-chain mRNA, clone AN05K.
DEFINITION M19909 J03832
ACCESSION M19909.1 GI:197025
VERSION C-region; immunoglobulin light chain; immunoglobulin-kappa-
KEYWORDS processed gene.
SOURCE Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Rule, G.S.
Unpublished (1988)
REFERENCE 2 (bases 1 to 458)
Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
AUTHORS Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies
TITLE for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
MEDLINE 88234486
PUBMED 3375235
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by

FEATURES
source Location/Qualifiers
1..458
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/strain="BALB/c"
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44..103
sig_peptide
mat_peptide
104..>458
/product="immunoglobulin kappa-chain"
BASE COUNT 108 a 105 c 119 g 126 t
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Query Match 85.0%; Score 371.6; DB 10; Length 458;
Best Local Similarity 94.1%; Pred. No. 3.6e-111;
Matches 386; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCAGTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGGATCTCT 83
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 32 CAAGTTCTCAGATGAGTCTCTCTCAGTTCCTGGGGTGCCTATGTTCTGGATCTCT 91
QY 84 GAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGTCACCTCTGGA 143
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 92 GGAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGTCACCTCTGGA 151
QY 144 GAATCAGTTTCCATCTCTCGAGTCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 203
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 152 GAATCAGTTTCCATCTCTCGAGTCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 211
QY 204 TACTTGAATGGTTTCTCAGAGACCAGGACAATCTCCTCAGCTCCTGATATTGATG 263
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 212 TACTTGAATGGTTTCTCAGAGACCAGGACAATCTCCTCAGCTCCTGATATTGATG 271
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTC 323
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 272 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTC 331
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 383
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 332 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 391
QY 384 GTAGAGTATCCATTACGTTCCGTCGGGGACAAAGTTGGAATAAAACG 433
II II IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 392 GTAGAGTTTCGGCTCACGTTCCGTCGGGACCAAGCTGGAGCTGAAACG 441

RESULT 5
MUSIGKAH 1400 bp DNA linear ROD 18-APR-1994
LOCUS Mouse Ig kappa active gene: v-kappa-167 v-j region.
DEFINITION J00553 J00563
ACCESSION J00553.1 GI:196735
VERSION C-region; J-region; V-region; complementarity determining region;
KEYWORDS framework region; hypervariable region; immunoglobulin light chain;
immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-24;
processed gene.
SOURCE hpcg22 & myelomas m511, m167 dna (see comment).
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 158 to 170; 537 to 617)
REFERENCE Joho, R., Weissman, I.L., Early, P., Cole, J. and Hood, L.
AUTHORS

```

TITLE Organization of kappa light chain genes in germ-line and somatic tissue

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (2), 1106-1110 (1980)

MEDLINE 80145717

PUBMED 6244580

REFERENCE 2 (bases 159 to 170; 537 to 847)

AUTHORS Garshenfeld,H.K., Tsukamoto,A., Weissman,I.L. and Joho,R.

TITLE Somatic diversification is required to generate the V kappa genes of MOPC 511 and MOPC 167 myeloma proteins

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (12), 7674-7678 (1981)

MEDLINE 82150933

PUBMED 6801657

REFERENCE 3 (bases 1 to 1400)

AUTHORS Gearhart,P.J. and Bogenhagen,D.F.

TITLE Clusters of point mutations are found exclusively around rearranged antibody variable genes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3439-3443 (1983)

MEDLINE 83221610

PUBMED 6222379

COMMENT the v-k167 gene codes for a v region which binds phosphocholine. all rearrangements of the v-k167 gene reported here are productive, and in all cases except hybridoma hpcg13 the codon at the site of recombination is ccg. in hpcg13 the codon is cct. the difference could be due to the variability of the v-j recombination site, or it could be an additional somatic mutation. [3] sequenced portions of the j-c intron and the c-kappa gene for all of its hybridomas and myelomas, and found no somatic mutation in these regions. [3] proposes a mechanism for the generation of clustered somatic mutation in the v-j region.

for the germline sequences of the v-k167 v and j regions see <musigkh2> <musigkhj2>. see loci beginning <musigk> for other rearranged kappa genes; see loci beginning <musigkj> for germline kappa v regions and see loci beginning <musigkj> for the germline kappa j and c regions. in the sites table cdr-complementarity determining region and fr-framework region.

Complete source information:

mouse cdna to myeloma m167 mrna [1],[2]; hybridomas hpcg9, hpcg10, hpcg13, hpcg22 & myeloma m511, m167 dna [3].

FEATURES

source 1..1400

Location/Qualifiers

organism="Mus musculus"

db_xref="taxon:10090"

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/notes="Ig V-K167 precursor"

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sig_peptide join(123..171,537..847)

mat_peptide /notes="Ig V-K167 signal pept"

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exon /product="Ig V-K167 mature v-j region"

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/number=1

Intron 172..536

/note="-k167 intron a"

variation 283

variation /notes="t in germline; g in hybridoma hpcg13"

variation 320

variation /note="c in germline; g in hybridoma hpcg10"

variation 376

variation /notes="a in germline; t in hybridoma hpcg13"

variation 391

variation /notes="t in germline; c in hybridoma hpcg13"

variation 409

variation /note="t in germline; c in myeloma m511"

variation 417

variation /notes="a in germline; g in myeloma m167"

variation 420

variation /note="a in germline; g in myeloma m167"

440 /note="a in germline; g in myeloma m167"

467 /note="a in germline; g in hybridoma hpcg13"

515 /note="c in germline; a in hybridoma hpcg13"

522 /note="t in germline; a in myeloma m511"

525 /note="c in germline; t in myeloma m511"

537..>884

/note="Ig V-K167 precursor"

/number=2

550 /note="t in germline; c in hybridoma hpcg13"

566 /note="g in germline; a in hybridoma hpcg13"

580 /note="t in germline; g in myeloma m511"

708 /note="a in germline; c in myeloma m167"

727 /note="a in germline; c in myeloma m167"

764 /note="g in germline; a in myeloma m167"

791 /note="a in germline; c in myeloma m167"

846..847

/organism="Mus musculus"

847 /note="g in hybridomas hpcg9, hpcg10, hpcg22 & comment)

511, m167; t in hybridoma hpcg13(see"

859 /note="t in germline; c in hybridoma hpcg10"

885..>1400

/note="v-k167 intron j-c"

895 /note="t in germline; c in hybridoma hpcg10"

1082 /note="a in germline; t in hybridoma hpcg13"

1085 /note="c in germline; t in myeloma m167"

1086 /note="t in germline; a in hybridoma hpcg10"

1096 /note="a in germline; c in hybridoma hpcg13"

1159 /note="t in germline; g in hybridoma hpcg10"

1229 /note="a in germline; g in hybridoma hpcg13"

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1279..1283

/note="tgaag in germline; tg in myeloma m511"

1289 /note="c in germline; t in hybridoma hpcg10"

BASE COUNT 399 a 250 c 350 g 401 t

ORIGIN unreported, chromosome 6.

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Best Local Similarity 95.5%; Pred. No. 1.5e-98;

Matches 343; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Db 531 TTTCAGAGTCAGTGGGATATTGTGATAACCCAGAGTCACTCTCCACTT 590

Qy 139 CTGGAGATCAGTTTCCATCTCTCAGGCTCTAGTAAGAGTCTCTGTATAGGATGGA 198

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591 CTGGAGAAATCAGTTTCCATCTCTCGAGGCTCTAGTAAGATCTCCTATATAAGGATGGGA 650
QY 199 AGACATACCTTGAATTTGTTCTCGAGAGACCAGGACAATCTCTCAGCTCCCTGATCTATT 258
Db 651 AGACATACCTTGAATTTGTTCTCGAGAGACCAGGACAATCTCTCAGCTCCCTGATCTATT 710
QY 259 TGATGTCACCCCGTGCAATCAGGAGTCTCAGACCCGGTTAGTGGCAGTGGGTTCAGGCACAG 318
Db 711 TGATGTCACCCCGTGCAATCAGGAGTCTCAGACCCGGTTAGTGGCAGTGGGTTCAGGCACAG 770
QY 319 ATTTCACCCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTACTGTCAAC 378
Db 771 ATTTCACCCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTACTGTCAAC 830
QY 379 AACTTGTAGATATCCATTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTACG 437
Db 831 AACTTGTAGATATCCCTCAGTTCGGTCTGGGACCAAGCTGGAGCTGAACAGTAAG 889

RESULT 6
MMU29425 339 bp mRNA linear ROD 03-FEB-1998
LOCUS Mus musculus anti-PC rearranged Ig kappa chain V-J region mRNA,
DEFINITION hybridoma 31-34-2, partial cds.
ACCESSION U29425
VERSION U29425.1 GI:2745913
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Guo,W.X., Burger,A.M., Fischer,R.T., Sieckmann,D.G., Longo,D.L. and
KENNY,J.J.
TITLE Sequence changes at the V-D junction of the VH1 heavy chain of
anti-phosphocholine antibodies alter binding to and protection
against Streptococcus pneumoniae
JOURNAL Int. Immunol. 9 (5), 665-677 (1997)
MEDLINE 97328374
PUBMED 9184912
REFERENCE 2 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
KENNY,J.J.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1995) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REFERENCE 3 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
KENNY,J.J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1998) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REMARK Nucleotide and protein sequence update by submitter
COMMENT On Jan 5, 1998 this sequence version replaced gi:903959.
FEATURES
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/db_xref="taxon:10090"
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/notes="hybridoma from spleen fused with SP2/0 myeloma"
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/db_xref="GI:2745914"
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FGSGPKLEIKR"
BASE COUNT 90 a 73 c 85 g 91 t
ORIGIN

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Query Match 74.8%; Score 326.8; DB 10; Length 339;
Best Local Similarity 97.9%; Pred. No. 2.1e-96;
Matches 331; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 96 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGATCACTTTCC 155
Db 1 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGATCACTTTCC 60
QY 156 ATCTCTCAGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 215
Db 61 ATCTCTCAGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 120
QY 216 TTCTCTCAGAGACCAAGCAATCTCTCAGCTCCCTGATGTATTGTATGCCACCGTGCA 275
Db 121 TTCTCTCAGAGACCAAGCAATCTCTCAGCTCCCTGATGTATTGTATGCCACCGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCCACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCCACCTGGAATC 240
QY 336 ACTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAACCTTGTAGATATCCA 395
Db 241 AGTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAACCTTGTAGATATCCT 300
QY 396 TTCACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 7
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LOCUS AR072863
DEFINITION Sequence 88 from patent US 5948658.
ACCESSION AR072863
VERSION AR072863.1 GI:9999626
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Landry,D.W.
TITLE Anti-cocaine catalytic antibody
JOURNAL Patent: US 5948658-A 88 07-SEP-1999;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 86 a 72 c 88 g 93 t
ORIGIN

Query Match 72.6%; Score 317.2; DB 6; Length 339;
Best Local Similarity 96.2%; Pred. No. 3.1e-93;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGATCACTTTCC 155
Db 1 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGATCACTTTCC 60
QY 156 ATCTCTCAGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 215
Db 61 ATCTCTCAGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 120
QY 216 TTCTCTCAGAGACCAAGCAATCTCTCAGCTCCCTGATGTATTGTATGCCACCGTGCA 275
Db 121 TTCTCTCAGAGACCAAGCAATCTCTCAGCTCCCTGATGTATTGTATGCCACCGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCCACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCCACCTGGAATC 240
QY 336 ACTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAACCTTGTAGATATCCA 395
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Db	241	AGTAGAGTGAAGGCTGAGGATGGGTGGCTATTACTGTCAACAATTTGTAGAGTATCCA	300
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RESULT 11			
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LOCUS	AR166319	420 bp	DNA
DEFINITION	Sequence 111 from patent US 6280987.		
ACCESSION	AR166319		
VERSION	AR166319.1	GI:16241586	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 420)		
AUTHORS	Landry,D.W.		
TITLE	Anti-cocaine catalytic antibody		
JOURNAL	Patent: US 6280987-A 111 28-AUG-2001;		
FEATURES	Location/Qualifiers		
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	/organism="unknown"		
BASE COUNT	98 a	95 c	115 g
ORIGIN		108 t	4 others
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Best Local Similarity		95.6%;	Pred. No. 7.9e-93;
Matches	325; Conservative	0;	Mismatches 15; Indels 0; Gaps 0;
Qy	94	GGGATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTT	153
Db	51	CGCATATGGTGATCACGACGAGTGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTT	110
Qy	154	CCATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT	213
Db	111	CCATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT	170
Qy	214	GGTTTCTGCAGACACGAGGACATCTCCTCAGCTCCTGTATTTGATGTCACCCCGTG	273
Db	171	GGTTTCTGCAGACACGAGGACATCTCCTCAGCTCCTGTATTTGATGTCACCCCGTG	230
Qy	274	CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAA	333
Db	231	CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAA	290
Qy	334	TCAGTAGAGTGAAGGCTGAGGATGGGTGCTGTATTTACTGTCAACACTTGTAGAGTATC	393
Db	291	TCAGTAGAGTGAAGGCTGAGGATGGGTGCTGTATTTACTGTCAACACTTGTAGAGTATC	350
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Db	351	CATTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAGC	390
RESULT 12			
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LOCUS	AR072865	368 bp	DNA
DEFINITION	Sequence 90 from patent US 5948658.		
ACCESSION	AR072865		
VERSION	AR072865.1	GI:9999628	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 368)		
AUTHORS	Landry,D.W.		
TITLE	Anti-cocaine catalytic antibody		
JOURNAL	Patent: US 5948658-A 90 07-SEP-1999;		
FEATURES	Location/Qualifiers		
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	/organism="unknown"		
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Query Match		70.8%;	Score 309.2; DB 6; Length 368;
Best Local Similarity		94.7%;	Pred. No. 1.4e-90;
Matches	320; Conservative	0;	Mismatches 18; Indels 0; Gaps 0;
Qy	96	GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTTCC	155
Db	1	GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTTCC	60
Qy	156	ATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG	215
Db	61	ATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG	120
Qy	216	TTTCTGCAGACACGAGGACAAATCTCCTCAGCTCCTGTATTTGATGTCACCCGTCGA	275
Db	121	TTTCTGCAGACACGAGGACAAATCTCCTCAGCTCCTGTATTTGATGTCACCCGTCGA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGGGTGCTGTATTTACTGTCAACACTTGTAGAGTATCCA	395
Db	301	TTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAGC	338
RESULT 13			
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LOCUS	AR166315	368 bp	DNA
DEFINITION	Sequence 103 from patent US 6280987.		
ACCESSION	AR166315		
VERSION	AR166315.1	GI:16241582	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 368)		
AUTHORS	Landry,D.W.		
TITLE	Anti-cocaine catalytic antibody		
JOURNAL	Patent: US 6280987-A 103 28-AUG-2001;		
FEATURES	Location/Qualifiers		
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	/organism="unknown"		
BASE COUNT	95 a	80 c	93 g
ORIGIN		100 t	
Query Match		70.8%;	Score 309.2; DB 6; Length 368;
Best Local Similarity		94.7%;	Pred. No. 1.4e-90;
Matches	320; Conservative	0;	Mismatches 18; Indels 0; Gaps 0;
Qy	96	GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTTCC	155
Db	1	GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTCTCTGGAGATCAGTTTCC	60
Qy	156	ATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG	215
Db	61	ATCTCCTCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG	120
Qy	216	TTTCTGCAGACACGAGGACAAATCTCCTCAGCTCCTGTATTTGATGTCACCCGTCGA	275
Db	121	TTTCTGCAGACACGAGGACAAATCTCCTCAGCTCCTGTATTTGATGTCACCCGTCGA	180
Qy	276	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC	335
Db	181	TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGGGTGCTGTATTTACTGTCAACACTTGTAGAGTATCCA	395

Db	241	AGTAGAGTGAAGCGTGGAGATGGGTGTGTATTACTTTCAACACTTTTGAAGACTATCCA	300
QY	396	TTACGTTTCGGCTCGGGGACAAAGTTGGAAATATAAACG	433
Db	301	TTACGTTTCGGCTCGGGGACAAATTTGGAGATAAACG	338
RESULT 14			
MMIG28			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
FEATURES			
Source			
mRNA			
CDS			
BASE COUNT	248 a	147 c	198 g 232 t
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Query Match			
Best Local Similarity	70.5%;	Score 308;	DB 10; Length 825;
Matches	311;	Conservative 0;	Mismatches 5; Indels 0; Gaps 0;
QY	79	TCTCTGAGTCAGTGGGGATATGTGTATACCCAGGATGAACCTCCAAATCCTGTCACTT	138
Db	309	TTTCAGGAGTCAGTGGGGATATGTGTATACCCAGGATGAACCTCCAAATCCTGTCACTT	368
QY	139	CTGGAGAATCAGTTTCCATCTCCTGCAGGTCCTAGTAAGAGTCTCCTGTATAAGGATGGGA	198
Db	369	CTGGAGAATCAGTTTCCATCTCCTGCAGGTCCTAGTAAGAGTCTCCTGTATAAGGATGGGA	428
QY	199	AGACATACCTTGAATTTGTTTCTGCAGAGACCCAGACAAATCTCCTCAGCTCCTGATGATT	258
Db	429	AGACATACCTTGAATTTGTTTCTGCAGAGACCCAGACAAATCTCCTCAGCTCCTGATGATT	488
QY	259	TGATGTCCACCCGTGCATCAGGAGTCTTCAGACCGGTTTACGTGGCAGTGGGTCAAGCACAG	318
Db	489	TGATGTCCACCCGTGCATCAGGAGTCTTCAGACCGGTTTACGTGGCAGTGGGTCAAGCACAG	548
QY	319	ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTCAGGATGTGGGTGTGTATTAAGTCAAC	378
Db	549	ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTCAGGATGTGGGTGTGTATTAAGTCAAC	608
QY	379	AACTTGTAGAGTATCC	394
Db	609	AACTTGTAGAGTATCC	624

Sat Apr 26 08:30:31 2003

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BASE COUNT      249 a      183 c      203 g      264 t
ORIGIN
Query Match      70.5%; Score 308; DB 10; Length 899;
Best Local Similarity 98.4%; Pred. No. 3.6e-90;
Matches 311; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 79 TCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTGCACATT 138
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   |||||||

QY 139 CTGGAGAAATCAGTTTCCATCTCTCGCAGGTCTAGTAAGAGTCTCCCTGTATAAGGATGGGA 198
   |||||||
Db 603 CTGGAGAAATCAGTTTCCATCTCTCGCAGGTCTAGTAAGAGTCTCCCTGTATAAGGATGGGA 662
   |||||||

QY 199 AGACATACTTGAATTGGTTTCTGCAGAGACCCAGGACAAATCTCCTCAGCTCCTGTATATT 258
   |||||||
Db 663 AGACATACTTGAATTGGTTTCTGCAGAGACCCAGGACAAATCTCCTCAGCTCCTGTATATT 722
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QY 259 TGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAG 318
   |||||||
Db 723 TGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAG 782
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QY 319 ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAAC 378
   |||||||
Db 783 ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAAC 842
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QY 379 AACTTGTAGAGTATCC 394
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Db 843 AACTTGTAGAGTATCC 858
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Job time : 875.354 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 578.185 seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttacattactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY_NUC
Gapop.10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba.*

2: em_esthma.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpi.*

7: em_estro.*

8: em_htc.*

9: gb_estl.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318.8	73.0	343	12 BF023001	BF023001 ux02c02.y
2	311.4	71.3	351	10 BB870732	BB870732 BB870732
3	290	66.4	906	12 BF785914	BF785914 602112548
4	281.2	64.3	400	10 AW912881	AW912881 uf46p05.y
5	280	64.1	935	11 BC031349	BC031349 Mus muscu
6	256	58.6	725	13 BG963055	BG963055 602828068

7	253.4	58.0	634	14 BM783161	BM783161 K-EST0061
8	251.8	57.6	522	13 BM511309	BM511309 ij46b08.y
9	250.2	57.3	751	12 BG542438	BG542438 602569513
10	250.2	57.3	787	12 BG536224	BG536224 602565445
11	250	57.2	995	14 BQ712430	BQ712430 AGENCOURT
12	249.2	57.0	491	12 BF174573	BF174573 MYF3409a
13	248.6	56.9	425	9 AA1734035	AA1734035 zu56d02.y
14	248.6	56.9	442	9 AA405415	AA405415 zu56d02.y
15	248.6	56.9	880	12 BG755003	BG755003 602711509
16	248.6	56.9	880	12 BG755003	BG755003 602711509
17	247.2	56.6	410	12 BG059215	BG059215 nah51g07.
18	246.2	56.3	382	9 AI882479	AI882479 uc02d02.r
19	245.4	56.2	643	14 BM820052	BM820052 K-EST0088
20	244	55.8	488	14 H25625	H25625 y148g05.r1
21	243.8	55.8	926	12 BG342051	BG342051 602463190
22	243	55.6	960	14 BQ711007	BQ711007 AGENCOURT
23	240.8	55.1	359	10 BB870575	BB870575 BB870575
24	240.8	55.1	770	12 BG530186	BG530186 602558684
25	240.8	55.1	990	13 B1838327	B1838327 603083265
26	240.6	55.1	701	12 BG547597	BG547597 602575437
27	240.6	55.1	774	13 BM007808	BM007808 603617276
28	239.8	54.9	427	12 BF174767	BF174767 MYE3784.M
29	238.4	54.6	614	10 AW405187	AW405187 UI-HF-BL0
30	237.4	54.3	462	12 BF176195	BF176195 MYB6594a
31	237.4	54.3	898	14 BQ708918	BQ708918 AGENCOURT
32	235.6	53.9	485	12 BF174421	BF174421 MYE3134a
33	234.8	53.7	424	12 BF176198	BF176198 MYB6598a
34	234.8	53.7	958	14 BQ709417	BQ709417 AGENCOURT
35	234.2	53.6	597	12 BF868788	BF868788 IL3-ETO11
36	234.2	53.6	650	13 B1765629	B1765629 603043768
37	233.8	53.5	952	12 BG758592	BG758592 6027112820
38	233.4	53.4	859	12 BG758795	BG758795 6027113155
39	232.6	53.2	816	13 B1759427	B1759427 603043095
40	232.6	53.2	908	12 BG685179	BG685179 602637065
41	231.8	53.0	783	12 BG541344	BG541344 602569848
42	231.2	52.9	421	14 BM894491	BM894491 ij65b10.y
43	231.2	52.9	421	14 BQ130227	BQ130227 ij82f03.y
44	231.2	52.9	421	14 BQ267173	BQ267173 ij98h05.y
45	231.2	52.9	421	14 BQ267663	BQ267663 ij92c11.y

ALIGNMENTS

RESULT 1	BF023001	ux02c02.y1	343 bp	mRNA	linear	EST 10-OCT-2000
LOCUS	BF023001	IMAGE:3470306 5'				Mus musculus cdna clone
DEFINITION	BF023001	V-II REGION VKAPPA167				PRECUSOR. i, mRNA sequence.
ACCESSION	BF023001	BF023001.1	GI:10754334			
VERSION	BF023001	EST.				
KEYWORDS	BF023001	house mouse.				
SOURCE	BF023001	Mus musculus				
ORGANISM	BF023001	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	BF023001	1 (bases 1 to 343)				
AUTHORS	BF023001	NCI-CGAP				http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	BF023001	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	BF023001	Unpublished (1997)				
COMMENT	BF023001	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1389666				
FEATURES	BF023001	Trace considered overall poor quality Seq primer: -40RP from Gibco High quality sequence stop: 1. Location/Qualifiers 1. .343 /organism="Mus musculus"				

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/sex="male"
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/dev_stage="4 weeks"
/lab_host="DH10B"
/notes: Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCATCTGAGTGGGAGCGCGGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      89 a      72 c      86 g      96 t
ORIGIN
Query Match      73.0%; Score 318.8; DB 12; Length 343;
Best Local Similarity 97.9%; Pred. No. 1.4e-86;
Matches 323; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 65 GCTTATGCTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTC 124
DB 13 GCTTATGCTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTC 72
QY 125 CAATCCGTCTCAGTCTGGAGAAATCAGTTCCTCCATCTCTCCAGTCTAGTAAGAGTCTCCT 184
DB 73 CAATCCGTCTCAGTCTGGAGAAATCAGTTCCTCCATCTCTCCAGTCTAGTAAGAGTCTCCT 132
QY 185 GTATAAGGATGGGAAGACATACCTTGAATGGTTTCTGCAGAGACCCAGGACAATCTCTCA 244
DB 133 ATATAAGGATGGGAAGACATACCTTGAATGGTTTCTGCAGAGACCCAGGACAATCTCTCA 192
QY 245 GCTCCGTGATGTTTGTATGTCACCGTGCATCAGAGTCTCAGACCGGTTAGTGGCAG 304
DB 193 GCTCCGTGATGTTTGTATGTCACCGTGCATCAGAGTCTCAGACCGGTTAGTGGCAG 252
QY 305 TGGGTACGGCAGCAGATTTACCTCCCTGAAATCAGTAGAGTGAAGGCTGAGAGTGTGGGTGT 364
DB 253 TGGGTACGAGACAGATTTACCTCCCTGAAATCAGTAGAGTGAAGGCTGAGAGTGTGGGTGT 312
QY 365 GTATTACTGTCAACACTTGTAGAGTATCC 394
DB 313 GTATTACTGTCAACACTTGTAGAGTATCC 342

RESULT 2
BB870732      351 bp      mRNA      linear      EST 27-NOV-2001
LOCUS      BB870732      RIKEN full-length enriched, adult male jejunal and colic
DEFINITION      lymph node Mus musculus cDNA clone G630024M15 5', mRNA sequence.
ACCESSION      BB870732
VERSION        BB870732.1      GI:17116942
KEYWORDS       EST.
SOURCE         house mouse.
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 351)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasake,N., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota
,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
```

```
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
Location/Qualifiers
1. 351
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G630024M15"
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and colic lymph node"
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dev_stage=16 days neonate, sex=mixed),
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BASE COUNT      89 a      77 c      87 g      98 t
ORIGIN
Query Match      71.3%; Score 311.4; DB 10; Length 351;
Best Local Similarity 96.7%; Pred. No. 2.6e-84;
Matches 318; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTTGGGGGTGCTTATGTTCTGATCTCT 83
DB 23 CAAGTTCTCAGAATGAGGTGCTCTCTTCAGTCTCTGGGGGTGCTTATGTTCTGATCTCT 82
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCCCAATCTCTGTCACCTTCTGGA 143
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QY 144 GAATCAGTTTCCATCTCTCTCGAGGTCCTAGTAAGAGTCTCTCTGTTATAAGGATGGGAAGACA 203
DB 143 GAATCAGTTTCCATCTCTCTCGAGGTCCTAGTAAGAGTCTCTCTATATAAGGATGGGAAGACA 202
QY 204 TACTTGAATGGTTCTTCAGACAGCAGGACAATCTCTCTCAGCTCCTCATGCTATTGTTG 263
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Db 263 TCACCCGTCATCAGGAGTCTCAGACCGTTTACTGGCAGTGGGTGAGAACAGATTTC 322
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGA 352
Db 323 ACCCTGGAATCAGTAGAGTGAAGCTGA 351

RESULT 3
BF785914
LOCUS BF785914
DEFINITION 602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
5', mRNA sequence.
ACCESSION BF785914
VERSION BF785914.1 GI:12090950
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 906)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: p column: 11
High quality sequence stop: 718.
FEATURES
    source
    Location/Qualifiers
        1..906
            /organism="Mus musculus"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:4240762"
            /clone_lib="NCI_CGAP_Kid14"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.75 kb. Constructed by Life
            Technologies. Note: This is a NCI_CGAP Library. |"
BASE COUNT 243 a 232 c 237 g 194 t
ORIGIN
Query Match 66.4%; Score 290; DB 12; Length 906;
Best Local Similarity 81.7%; Pred. No. 1.3e-77;
Matches 335; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATGAGGTTCTCTGTTTCAGTTTCGGGGTGCCTTATGTTCTGGATCTCT 83
Db 3 CAAAGTTCTCAGATAGAGGTCCTAGCTAGTGTTCCTGGGGTCTGTTGCTCTGGATCCTCT 62
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCCAAATCCTCTCACTCTCTGGA 143
Db 63 GGAGCATTTGGGATATTGTGATGACTCAGGCTGTACCCCTCTGCTACCTCTCACTCTGGA 122
QY 144 GAATCAGTTTCCATCTCTGCGAGGTTCTAGTAAGAGTCTCTCTGATAAGGATGGGAAGACA 203
Db 123 GAGTCAGTATCCATCTCTCTGCAGGTTCTAGTAAGAGTCTCTCTGATAAGGATGGGATG 182
QY 204 TACTTCAATTTGGTTCTGCGAGAGACCAGACAAATCTCTCACTCTCTGATGATTGATG 263
Db 183 GACTTGTATTTGGTTCTACAGAGGCCAGGCCAGTCTCTCTCACTCTCTGATATATCGGATG 242
QY 264 TCACCCGTCATCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTC 323
Db 243 TCCAACTTGCCTCAGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTGAGGACAGTCTCTTC 302
```

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QY 324 ACCCTGGAATCAGTAGAGTGAAGCTCAGGATGTGGTGTGTTATTACTCTCAACACTT 383
Db 303 ACACAGATCAGTACAGTAGGAGGCTGAGATGTGGTGTATTATTCTTTGCAACAT 362
QY 384 GTAGAGTATCCATTACAGTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 363 CTAGAATATCGTACAGTTCGGAGGGGGACCAAGCTGGAATAAAACG 412

RESULT 4
AW912881
LOCUS AW912881
DEFINITION uf46b05.y1 Soares_mammary_gland_NMLMG Mus musculus linear EST 25-MAY-2000
IMAGE:1514385 5' similar to gb:J00560 mouse ig kappa mrna from
mopc21 & other myeloma mrna 3' (MOUSE);, mRNA sequence.
ACCESSION AW912881
VERSION AW912881.1 GI:8078508
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 400)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:941237
Seq primer: -40RP from Gibco.
FEATURES
    source
    Location/Qualifiers
        1..400
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone="IMAGE:1514385"
            /clone_lib="Soares_mammary_gland_NMLMG"
            /sex="female (lactating)"
            /tissue_type="mammary gland"
            /lab_host="DH10B"
            /note="Vector: pT73D-Pac (Pharmacia) with a modified
            polylinker; 1st strand cDNA was prepared from mammary
            gland tissue from a lactating female, and was then primed
            with a Not I - oligo(dT) primer. Double-stranded cDNA was
            ligated to Eco RI adaptors (Pharmacia), digested with Not
            I and cloned into the Not I and Eco RI sites of the
            modified pT73 vector. Library is normalized. Library
            was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 90 a 90 c 110 g 110 t
ORIGIN
Query Match 64.3%; Score 281.2; DB 10; Length 400;
Best Local Similarity 81.7%; Pred. No. 4.7e-75;
Matches 325; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCGGGGTGTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db 2 ATTCGGTAGAGGCTGTTTTCGGGGTGTCTGTGCTCTGGATCCTCGAGGCAATTGGG 61
QY 96 GATATTGTGATACCCAGGATGAACCTCCAAATCCTCTCACTCTCTGGAGATCAGTTTCC 155
Db 62 GATATTGTGATGACTCAGGCTGCACCCCTCTCTACTCTCTCGAGATCAGTATCC 121
QY 156 ATCTCTCGAGGCTTAGTAAGAGTCTCTCTGTATAGGATGGGAGACATCTGTAATGG 215
Db 122 ATCTCTCGAGGCTTAGTAAAAGTCTCTGTCATATTGATGGCAACACTTATTATATGG 181
QY 216 TTTCTGAGAGACACAGACAAATCTCTCAGTCTCTGATGATTGATGTCACCCGTCGA 275
Db 182 TTCTGCGAGAGGCCAGGCCAGTCTCTCAGCTCTGATATATCGGATGTCCAACCTTGTG 241
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QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTCACCCCTGGAATC 335
 Db 242 TCAGAGTCCACAGACAGGTTTCAGTGGCAGTGGGTTCAGGAACTGCTTTCACACTGAGAATC 301
 QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
 Db 302 AGTAGAGTGAAGGCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCA 361
 QY 396 TTCAGTTCGGCTCGGGGCAACAAGTTGGAATAAAACG 433
 Db 362 TACACGTTCCGAGGGGGACCAAGCTGGAATAAAACG 399

BC031349 935 bp mRNA linear HTC 03-JUN-2002
 LOCUS Mus musculus, clone IMAGE:1514385, mRNA.
 ACCESSION BC031349
 VERSION BC031349.1 GI:21315064
 KEYWORDS HTC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 935)
 Strausberg, R.
 Direct Submission
 Submitted (03-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NTH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Marcello Bento Soares, Ph.D.
 cDNA Library Preparation: Soares Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 67 Row: j Column: 4
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein
 This clone has the following problem: no cloning site /
 microdeletion.

FEATURES
 source
 1..935
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1514385"
 /tissue_type="Mammary gland, lactating mouse"
 /clone_lib="Soares_mammary_gland_NMLMG"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac"
 BASE COUNT 251 a 247 c 208 g 229 t
 ORIGIN

Query Match 64.1%; Score 280; DB 11; Length 935;
 Best Local Similarity 83.1%; Pred. No. 1.5e-74;
 Matches 319; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 50 TCAGTTTCTGGGGGTCTTATGTTCTGGATCTCTGAGTCTAGTGGGATATTGTGATAC 109
 Db 2 TGAGTTCTCCGGGGTCTCTTGTCTCTGGATCCTCGAGCCATTGGGGATATTGTGATGAC 61
 QY 110 CCAGGATGAACCTCTCAATCCCTGTCACCTCTCTCGAGAACTCAGTTTCCATCTCCTCGAGGTC 169
 Db 62 TCAGGCTGCACCCCTCTGTACCTCTCCTCGAGAGTCAGTATCCATCTCCTCGAGGTC 121
 QY 170 TAGTAAGATCTCCCTGTATTAAGGATGGGAAGATACATTGAATTGGTTTCTCGAGAGACC 229
 Db 122 TAGTAAAGTCTCCCTGCATATTGATGGCAACACTTATTATTATTTGTTCTCGAGAGGCC 181
 QY 230 AGACAATCTCTCAGCTCTGATGTTATTTGATGCCACCCCTGATCAGGAGTCTCAGA 289
 Db 182 AGCCAGTCTCCTCAGCTCTGATATATCGGATGTCACAACTTGTCTCAGGAGTCCCGCA 241
 QY 290 CCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTCCACCCTGGAAATCAGTAGAGTCAAGGC 349
 Db 242 CAGGTTTCAGTGGCAGTGGGTGAGGAACTGCTTTCACACTGGAATCAGTAGAGTGGAGGC 301
 QY 350 TGAGGATGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCATTACGTTCCGGCTC 409
 Db 302 TGAGGATGGGTGTTTACTGTATGCAACATCTAGAAATATCCGACGTTCCGGAGG 361
 QY 410 GGGGACAAAGTTGGAAATAAAACG 433
 Db 362 GGGGACCAAGCTGGAATAAAACG 385

RESULT 6
 LOCUS BG963055
 DEFINITION 602828068F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5',
 mRNA sequence.
 ACCESSION BG963055
 VERSION BG963055.1 GI:14350692
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 725)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10986 row: g column: 18
 High quality sequence stop: 719.
 Location/Qualifiers
 1..725
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4982825"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: Notf;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 195 a 182 c 174 g 174 t
 ORIGIN

Query Match 58.6%; Score 256; DB 13; Length 725;
 Best Local Similarity 79.8%; Pred. No. 3e-67;

Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@oeb.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excision to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
seq primer: -40RP from G1bco
High quality sequence stop: 429.

FEATURES

source

1. 522

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:563990"

/clone_lib="Human insulinoma"

/tissue_type="insulinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZAPIT system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excision to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

109 a 142 c 136 g 135 t

BASE COUNT

ORIGIN

Query Match 57.6%; Score 251.8; DB 13; Length 522;

Best Local Similarity 76.2%; Pred. No. 5e-66;

Matches 310; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 30 CTCACATGAGTCTCTGTTTCAGTTCTGGGGTCTTATGTTCTGATCTCTGGAGTC 89

DB 14 CTCACATGAGTCTCTGTTTCAGTCTGGGGTCTTATGTTCTGATCTCTGGAGTC 73

QY 90 AGTGGGATATTGTGATACCCAGGATGAAGTCTCCAACTCTGTCATCTCTGGAGTCA 149

DB 74 AGTGGGATATTGTGATACCCAGGATGAAGTCTCCAACTCTGTCATCTCTGGAGTCA 133

QY 150 GTTTCATCTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 209

DB 134 GCTCCATCTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 193

QY 210 AATTGGTTTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 269

DB 194 GATTGTACTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 253

QY 270 CCGTATCAGGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 329

DB 254 CGGGCTCGGGGTCCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 313

QY 330 GAATCAGTATGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 389

DB 314 AACATCAGCAGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 373

QY 390 TATCCATTCAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 436

DB 374 ACTCGGTGACGTTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 420

RESULT 9

BG542438

LOCUS

DEFINITION BG542438 751 bp mRNA linear EST 03-APR-2001

602569513f1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694091 5',

mRNA sequence.

ACCESSION BG542438

VERSION BG542438.1 GI:13534671

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 751)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs@xmail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMI517 row: i column: 04

High quality sequence stop: 737.

FEATURES

source

1. 751

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4694091"

/clone_lib="NIH_MGC_77"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggccctcgcc); Site:2: SfiI (ggccattatg); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH-MGC Library."

181 a 211 c 198 g 161 t

Query Match 57.3%; Score 250.2; DB 12; Length 751;

Best Local Similarity 75.9%; Pred. No. 1.8e-65;

Matches 309; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 30 CTCACATGAGTCTCTGTTTCAGTTCTGGGGTCTTATGTTCTGATCTCTGGAGTC 89

DB 26 CTCACATGAGTCTCTGTTTCAGTCTGGGGTCTTATGTTCTGATCTCTGGAGTC 85

QY 90 AGTGGGATATTGTGATACCCAGGATGAAGTCTCCAACTCTGTCATCTCTGGAGTCA 149

DB 86 AGTGGGATATTGTGATACCCAGGATGAAGTCTCCAACTCTGTCATCTCTGGAGTCA 145

QY 150 GTTTCATCTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 209

DB 146 GCTCCATCTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 205

QY 210 AATTGGTTTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 269

DB 206 GATTGTACTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 265

QY 270 CCGTATCAGGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 329

DB 266 CGGGCTCGGGGTCCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 325

QY 330 GAATCAGTATGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 389

DB 326 AAAATCAGCAGAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 385

QY 390 TATCCATTCAGTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 436

DB 386 ACTCGGTGACGTTCTGAGAGTCTAGTAAAGTCTCTGTTATAGGATGGAGACATCTTG 432

RESULT 10

BG536224

LOCUS BG536224 787 bp mRNA linear EST 03-APR-2001
 DEFINITION 602565445F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690258 5',
 mRNA sequence.
 ACCESSION BG536224
 VERSION BG536224.1 GI:13527769
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 787)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLC1507 row: i column: 11
 High quality sequence stop: 721.
 Location/Qualifiers
 1..787
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4690258"
 /clone_lib="NIH_MGC_77"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccctcgccc); Site_2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTATAGAGCGGAGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."
 BASE COUNT 196 a 213 c 188 g 190 t
 ORIGIN
 Query Match 57.3%; Score 250.2; DB 12; Length 787;
 Best Local Similarity 75.9%; Pred. No. 1.8e-65;
 Mismatches 0; Mismatches 98; Indels 0; Gaps 0;
 Matches 309; Conservative 0;
 QY 30 CTCACATGAGTTCTCTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCTGGAGTC 89
 Db 26 CTCACATGAGTTCTCTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCTGGAGTC 85
 QY 90 AGTGGGATATTGTGATACCCAGGATGAACCTCCATCTCTGTCACCTTCACCTTCGGAGAATCA 149
 Db 86 AGTGGGATATTGTGATGACTGACTCCATCTCCCTGCCGTGACCCCTCGAGAGCGG 145
 QY 150 GTTTCATCTCTGAGGCTAGTAGAGTCTCTGTATAGGATGGAAGACATCTTG 209
 Db 146 GCCTCATCTCTGAGGCTAGTAGAGTCTCTGTATAGGATGGAAGACATCTTG 205
 QY 210 AATTGTTTCTGAGAGCAGGACAACTCTCTCAGCTCTCTGATGATTTGATGCCACC 269
 Db 206 GATTGTTCTGAGAGCAGGACAACTCTCTCAGCTCTCTGATGATTTGATGCCACC 265
 QY 270 CGTGCAATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTAGGACAGATTTTACCCCTG 329
 Db 266 CGGGCTCCGGGCTCCCTGACAGGTTTCAGTGGCAGTGGATGAGGACAGATTTTACCTG 325
 QY 330 GAATCAGTAGAGTGAAGCTGAGGATGTTGGGTGCTGATTTACTGTCAACAACCTTGTAGAG 389
 Db 326 AAAATCAGTAGAGTGAAGCTGAGGATGTTGGGTGCTGATTTACTGTCAACAACCTTGTAGAG 385

QY 390 TATCCATTACGTTCTGGTCTGGGGACAAAGTTTGGAAATAAAACGTAC 436
 Db 386 ACTCTAGGACCTTCGCCAAGGACACGACTGGAGATTAAACGAAC 432
 RESULT 11
 LOCUS B0712430
 DEFINITION 5' mRNA sequence.
 ACCESSION B0712430
 VERSION B0712430.1 GI:21851329
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 995)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2464 row: j column: 02
 High quality sequence stop: 645.
 Location/Qualifiers
 1..995
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6277729"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 BASE COUNT 242 a 273 c 252 g 227 t 1 others
 ORIGIN
 Query Match 57.2%; Score 250; DB 14; Length 995;
 Best Local Similarity 76.4%; Pred. No. 2.3e-65;
 Mismatches 0; Mismatches 95; Indels 0; Gaps 0;
 Matches 307; Conservative 0;
 QY 35 CATGAGTTCTCTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGG 94
 Db 6 CATGAGTTCTCTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGG 65
 QY 95 GGATATTGTATACCCAGGATGAACCTCTCAATCTCTGTCAGTCTCTGGAATCAGTTTC 154
 Db 66 GGATATTGTATGACTCAGTCTCCACTCTCCCTGCCGTGACCCCTGGAGCGGCTC 125
 QY 155 CATCTCTGCAAGTCTAGTAGAGTCTCTGATATAGGATGGGAAGACATCTTGAATG 214
 Db 126 CATCTCTGCAAGTCTAGTAGAGTCTCTGATATAGGATGGGAAGACATCTTGAATG 185
 QY 215 GTTCTGCAAGACCCAGGACAACTCTCTCAGTCTCTGATGATTTGATGCCACCCTGC 274
 Db 186 GTACTCTGCAAGACCCAGGACAACTCTCTCAGTCTCTGATGATTTGATGCCACCCTGC 245
 QY 275 ATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTTACCTGGAAT 334
 Db 246 CTCGGGGTCTCTGACAGGTTTCAGTGGCAGTGGGATGAGGACAGATTTTACATGAAAT 305

Qy	335	CAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTTGAGAGTACC	394
Db	306	CAGCAGAGCTGAGGCTGAGGATGTGGGGTTTATTACTGCATGCAAGCTCTACAACCTCC	365
Qy	395	ATTACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAAACGTAC	436
Db	366	GTAACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAAC	407

RESULT 12	Bf174573	491 bp	mRNA	linear	EST 23-MAR-2001
LOCUS	MYE3409a	Myeloma (MYE)	cDNA library	Homo sapiens	cdNA, mRNA
DEFINITION	Bf174573	sequence.			
ACCESSION	Bf174573				
VERSION	Bf174573.1	GI:13440787			
KEYWORDS	EST.				
SOURCE	human..				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 TO 491)				
JOURNAL	Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Cukerman,E.,				
COMMENT	Franciso-Pabalan,O., Liew,C.C. and Stewart,A.K. The transcriptional phenotype of myeloma cells Unpublished (2000) Contact: A. Keith Stewart, M.D. Oncology Research University Health Network 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada Tel: (416) 946-4639 Fax: (416) 946-6546 Email: k.stewart@utoronto.ca PCR Primers FORWARD: 5'-GCCAAGTCGAAATTAACCCCTACTAAAGG-3' BACKWARD: 5'-CCAGTGAATTTGAATACCGACTCACTATAGGGC-3' Seq primer: 5'-GAAATTAACCCCTCACTAAAGG-3'.				

FEATURES
source

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FEATURES
source
Location/Qualifiers
1. .491
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Myeloma (MYE) cDNA library"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="multiple myeloma"
/note="Vector: Lambda Zap Express; Site 1: EcoRI; Site 2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(T)18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MuV reverse transcriptase. To protect the cDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32P]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
EcoRI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The cDNAs were then
size-fractionated using Sephacryl S-500 column and then
ligated into EcoRI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using Gigapack
II packaging extract. The library had primary titre of
approx. 1x106. Clones from the primary library were
randomly selected for single pass sequencing."
102 a 136 c 128 g 124 t 1 others
BASE COUNT
ORIGIN
Query Match 57.0%; Score 249.2; DB 12; Length 491;
Best Local Similarity 75.7%; Pred. No. 3,1e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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[illegible]

RESULT	13
AI734035	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>

JOURNAL
COMMENT

COURT
COMMENT

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>...</i>	
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100. <i>...</i>	

source

Source

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

```

BASE COUNT      88 a 114 c 111 g 112 t
ORIGIN

Query Match      56.9%; Score 248.6; DB 9; Length 425;
Best Local Similarity 75.7%; Pred. No. 4.4e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 30 CTCACATGAGGTTCTCTGTTTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
    ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGGCTGTAATGCTCTGGTCTCTGGATCC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 AGTGGGGATATTGTGATACCCAGGATGACCTCCATCTCCATCTCTGTCACCTCTGGAGAATCA 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75 AGTGGGGATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGCTCATCTCCCTGGAGAGCCG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 GTTTCATCTCTCGAGGCTAGTAGAGTCTCCTGTATAGGATGGGAAGACATACCTTG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 135 GCCTCATCTCTGCAAGTCTAGTCAGAGCCCTCCTGCTTAGTAAATGGATATAATTATTG 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 AATTGGTTTCTGAGAGACAGGACAATCTCTCAGCTCCTGATGATATTGATGTCACC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 GATTGGTATCTGCAGAAGCAGGGCAGTCTCCACAGCTCCTGATCTATTTTGGGTTCTAAT 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 CGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 CGGGCTCCGGGTCCTCAGAGTTTACAGAGTTTACAGTGGATCAGGACAGATTTTACATG 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 GAAATCAGTAGAGTGAAGGCTAGTAGAGTCTCTGATGATGATGATGATGATGATGATGATG 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 ARAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATCACTGATGATGATGATGATGATG 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 TATCCATTACGTTGCGGTCGGGACAAAGTTGGAAATAAAACGTCAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 TCTCCTCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAACGAAC 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AA05415      442 bp mRNA linear EST 09-NOV-1997
LOCUS      zu56d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:741987 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II
REGION (HUMAN);, mRNA sequence.
ACCESSION  AA05415
VERSION     AA05415.1 GI:2063652
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 442)
AUTHORS    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krieman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE      WashU-NCI human EST Project
JOURNAL    Unpublished (1997)
COMMENT     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1053 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES
source      Location/Qualifiers
            1..442
            /organism="Homo sapiens"

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/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone="IMAGE:741987"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      90 a 120 c 114 g 118 t
ORIGIN

Query Match      56.9%; Score 248.6; DB 9; Length 442;
Best Local Similarity 75.7%; Pred. No. 4.5e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 30 CTCACATGAGGTTCTCTGTTTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGGCTGTAATGCTCTGGTCTCTGGATCC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 AGTGGGGATATTGTGATACCCAGGATGACCTCCATCTCCTGTCACCTCTGGAGAATCA 149
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Db 75 AGTGGGGATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGCTCATCTCCCTGGAGAGCCG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 GTTTCATCTCTCGAGGCTAGTAGAGTCTCCTGTATAGGATGGGAAGACATACCTTG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 135 GCCTCATCTCTGCAAGTCTAGTCAGAGCCCTCCTGCTTAGTAAATGGATATAATTATTG 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 AATTGGTTTCTGAGAGACAGGACAATCTCTCAGCTCCTGATGATGATGATGATGATGATGATG 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 GATTGGTATCTGCAGAAGCAGGGCAGTCTCCACAGCTCCTGATCTATTTTGGGTTCTAAT 254
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QY 270 CGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 CGGGCTCCGGGTCCTCAGAGTTTACAGAGTTTACAGTGGATCAGGACAGATTTTACATG 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 GAAATCAGTAGAGTGAAGGCTAGTAGAGTCTCTGATGATGATGATGATGATGATGATGATG 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 ARAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATCACTGATGATGATGATGATGATG 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 TATCCATTACGTTGCGGTCGGGACAAAGTTGGAAATAAAACGTCAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 TCTCCTCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAACGAAC 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
EG755003      880 bp mRNA linear EST 15-MAY-2001
LOCUS      602711509f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851723 5',
DEFINITION mRNA sequence.
ACCESSION  EG755003
VERSION     EG755003.1 GI:14065656
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 880)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LNL)

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CMI695 row: a column: 04
High quality sequence stop: 845.
Location/Qualifiers
1. .880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4851723"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 204 a 266 c 216 g 194 t
ORIGIN
Query Match 56.9%; Score 248.6; DB 12; Length 880;
Best Local Similarity 75.7%; Pred. No. 5.9e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 30 CTCACCATGAGTTCCTGTGTTCTGGGGTGGTATGTTCTGGATCTCTGGAGTC 89
Db 5 CTCACATGAGGCTCCTGCTCAGCTCTGGGGTGGTAAATGCTGGGTCTCTGGATCC 64
QY 90 AGTGGGATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCTCTGGAGATCA 149
Db 65 AGTGGGAAATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGCCG 124
QY 150 GTTTCATCTCCTCCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTG 209
Db 125 GCCTCCATCTCCTCGAGGTCTAGTCAGAGCTCTGTCAGAGCTCTGTCATAGCAATGGATACACCTATTG 184
QY 210 AATTGGTTTCTGCAGACCCAGGACAACTCTCCTCAGCTCTGTATTTGATGTCAC 269
Db 185 GATTGGTACCTGCAGAGCGGGGCGAGTCTCCACACTCTATTTGGGTCTAAT 244
QY 270 CGTGCATCAGAGTCTCAGACCGGTTTATGGCAGTGGGTTCAGGCACAGATTTACCCCTG 329
Db 245 CGGCGCTCCGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTG 304
QY 330 GAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACTTTGAGAG 389
Db 305 AAGATCAACAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAA 364
QY 390 TATCCATTACGTTCCGCTCGGGACAAAGTTGGGAATAAAACGTAC 436
Db 365 ACTCCCTTCACTTCGGCCCTGGGACCAAAAGTGGAAATCAACGAAC 411

Search completed: April 26, 2003, 07:26:43
Job time : 585.185 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 87.9172 Seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttacagttactcagc.....agttggaaataaacgtacg 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	437	100.0	437	21	AAZ34746
2	366.4	83.8	429	12	AAQ12056
3	366.4	83.8	429	12	AAQ12012
4	317.2	72.6	340	19	AAV09791
5	317.2	72.6	368	19	AAV09789
6	316	72.3	420	19	AAV09802
7	309.2	70.8	368	19	AAV09793
8	293.2	67.1	464	14	AAQ33097
9	293.2	67.1	464	14	AAQ36950

10	286.8	65.6	961	16	AAQ79929	Anti-tobacco mosai
11	277.2	63.4	441	11	AAQ08602	B38.1 Light Chain
12	277.2	63.4	441	18	AAV74344	MAB B38-1 light ch
13	277.2	63.4	441	20	AAV71152	Coding strand for
14	276.4	63.2	399	14	AAQ38878	CTMO1 VL cDNA. Sy
15	276.4	63.2	399	18	AAQ38878	Anti-HMFG MAB CTMO
16	276.4	63.2	399	21	AAZ46913	MAB CT-M-01 light
17	271.4	62.1	720	21	ABK10999	DNA encoding prote
18	257.2	58.9	348	21	AAZ34747	Humanised anti-CD2
19	255.6	58.5	720	21	AAAL3924	Human PTHR-P monoc
20	255	58.4	772	20	AAZ24418	Human bladder tumo
21	254.6	58.3	720	21	AAAL3927	Human PTHR-P monoc
22	253	57.9	720	21	AAAL3926	Human PTHR-P monoc
23	252.2	57.7	720	21	AAAL3925	Human PTHR-P monoc
24	251.8	57.6	720	21	AAAL3928	Human PTHR-P monoc
25	251.6	57.6	651	20	AAZ24421	Human bladder tumo
26	251.2	57.5	720	21	AAAL3920	Human PTHR-P monoc
27	251	57.4	793	24	ABK43188	DNA encoding const
28	250.8	57.4	720	21	AAAL3922	Human PTHR-P monoc
29	250.8	57.4	720	21	AAAL3923	Human PTHR-P monoc
30	250	57.2	501	20	AAZ57787	Anti-HCV Ser/Thr p
31	250	57.2	1111	24	ABK43191	DNA encoding fiber
32	250	57.2	1402	24	ABK43192	DNA encoding fiber
33	249.6	57.1	336	21	AAZ38897	2G3 hybridoma VL d
34	249.4	57.1	963	22	AAZ44895	Human breast cance
35	249	57.0	720	21	AAAL3921	Human PTHR-P monoc
36	248.4	56.8	339	21	AAQ09017	Murine 13H10 light
37	243.4	55.7	373	19	AAV18472	TAL antibody VL ch
38	242.4	55.5	720	21	AAAL3929	Human PTHR-P monoc
39	238.4	54.6	882	15	AAQ73406	81C6 light chain v
40	236.2	54.1	417	22	AAH41159	Human coding seque
41	234.2	53.6	891	19	AAV66632	Human immunoglobul
42	234.2	53.6	891	21	AAZ78320	Anti-human Fas Ig
43	231.8	53.0	1497	24	AAZ97145	3B10xP4-3 bispecif
44	231.8	53.0	1509	24	AAZ97146	3B10xP4-14 bispecif
45	231.8	53.0	1509	24	AAZ97147	3B10xP5-2 bispecif

ALIGNMENTS

RESULT 1
AAZ34746
ID AAZ34746 standard; cDNA; 437 BP.
XX
AC AAZ34746;
XX
DT 15-FEB-2000 (first entry)
DE Mouse anti-CD23 MAB C11 light chain variable region cDNA.
XX
CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.
XX
OS Mus musculus.

XX	Key	Location/Qualifiers
FT	CDS	3..413
FT		/*tag= a
XX		
PN	WO9958679-A1.	
XX		
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999;	99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.
XX (GLAX) GLAXO GROUP LTD.
XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX WPI; 2000-053101/04.
XX P-PSDB; AAY32261.
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX Claim 16; Fig 2; 81pp; English.
XX This DNA sequence encodes the light chain variable region (VL) of
XX murine anti-CD23 (FCERI) monoclonal antibody C11. The invention
XX provides altered antibodies, such as chimeric or humanised
XX antibodies (see AAZ34747 and AAZ34748), which comprise sufficient of
XX the amino acid sequences of the C11 light and heavy chain
XX complementary determining regions (see AAY32254-59) to render them
XX capable of binding to the CD23 type II molecule expressed on
XX haematopoietic cells. The antibodies are used to block soluble
XX CD23 formation in human therapy, for the treatment of arthritis,
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
XX asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
XX eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
XX (particularly chronic bronchitis) or diabetes (particularly type 1
XX diabetes), and B-cell malignancies (claimed). They are also useful
XX for studying interactions between CD23 and various ligands and
XX determining the binding agents.
XX Sequence 437 BP; 108 A; 93 C; 114 G; 122 T; 0 other;

Query Match 100.0%; Score 437; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.6e-124;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGTTCTCTGTTCAGTTCTGG 60
Db 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGTTCTCTGTTCAGTTCTGG 60
Qy 61 GGGTCTTATGTTCTGGATCTCTGGATCAGTGGGGATATTGTGATAACCCAGGATGAAC 120
Db 61 GGGTCTTATGTTCTGGATCTCTGGATCAGTGGGGATATTGTGATAACCCAGGATGAAC 120
Qy 121 TCTCAATCCCTGTCACCTTCTGGAGAATCAGTTTCCATCTCTCGAGTCTAGTAAGATC 180
Db 121 TCTCAATCCCTGTCACCTTCTGGAGAATCAGTTTCCATCTCTCGAGTCTAGTAAGATC 180
Qy 181 TCCTGTATAGGATGGAAGACATACCTTGAATGTTTCTGCAGACACCAAGCAATCTC 240
Db 181 TCCTGTATAGGATGGAAGACATACCTTGAATGTTTCTGCAGACACCAAGCAATCTC 240
Qy 241 CTCAGTCCCTGATGATTTGATGTCACCCGTCGATCAGAGTCTCAGACCGTTTAGTG 300
Db 241 CTCAGTCCCTGATGATTTGATGTCACCCGTCGATCAGAGTCTCAGACCGTTTAGTG 300
Qy 301 GCAGTGGGTCTAGGCACAGATTTTCACTCCCTGGAAATCAGTAGAGTGAAGCTGAGGATG 360
Db 301 GCAGTGGGTCTAGGCACAGATTTTCACTCCCTGGAAATCAGTAGAGTGAAGCTGAGGATG 360
Qy 361 GTGTGTTATTACTGTCAACAACATTTGATAGAGTATCCATTACGTTTCGGCTCGGGGACAAAGT 420
Db 361 GTGTGTTATTACTGTCAACAACATTTGATAGAGTATCCATTACGTTTCGGCTCGGGGACAAAGT 420
Qy 421 TGGAAATAAACAACGTACG 437
Db 421 TGGAAATAAACAACGTACG 437

RESULT 2
AAQ12056
ID AAQ12056 standard; DNA; 429 BP.
XX
XX AAQ12056;
XX
XX 15-AUG-1991 (first entry)
XX
XX Sequence encoding light (kappa) chain variable region of murine
XX 2E12 immunoglobulin.
XX
XX Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 34..429
XX /tag= a
XX /product= mouse MAb 2E12 L(kappa)-chain
XX variable region
XX
XX WO9107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1990; 90WO-US06615.
XX
XX 13-NOV-1989; 89US-0433730.
XX
XX (XOMA-) XOMA CORP.
XX (GREC) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX
XX WPI: 1991-178044/24.
XX P-PSDB; AAR12354.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and
XX remove HIV-1 antigen from sample
XX
XX Disclosure; fig 1: 107pp; English.
XX
XX This sequence encodes the light (kappa)- chain variable (V) region
XX of a mouse monoclonal antibody (MAb), 2E12, specific for an HIV-1
XX viral antigen. It is used in the construction of a chimeric MAb
XX comprising heavy and light chains having murine V regions and human
XX C regions. The chimeric MABs are more effective than murine MAB
XX 2E12 since they have an increased compatibility in humans. The
XX heavy and light chain V-regions are joined by manipulating their
XX respective joining (J) regions, to generate restriction enzyme
XX recognition sites. The chimeric MABs can be used as immuno-
XX conjugates, in association with e.g. toxins for HIV treatment.
XX See also AAQ12057-63.
XX
XX Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 other;

Query Match 83.8%; Score 366.4; DB 12; Length 429;
Best Local Similarity 93.6%; Pred. No. 1.7e-102;
Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 24 CAGGACCTCACCATGAGTTCTCTGTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCT 83
Db 22 CAAGTTCTCAGAAATGAGTGGTCTCTCTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCT 81
Qy 84 GGAGTCAGTGGGGATATTCTGATAACCCAGGATGAACCTCCTCAATCCTGTCACCTTCTGGA 143
Db 82 GGAGTCAGTGGGGATATTCTGATAACCCAGGATGAACCTCCTCAATCCTGTCACCTTCTGGA 141
Qy 144 GAATCAGTTTCCATCTCTCGAGGCTTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 203
Db 142 GAATCAGTTTCTCTCTCGAGGCTTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 201

QY 204 TACTTGAATGGTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGATTTGATG 263
 Db 202 TACTTGAGTTGGTTCTGCAGAGACCAGGACAATCTCCGAGCTCCTGATCTATCTGATG 261
 QY 264 TCCACCCGTCGATCAGAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGACAGATTTTC 323
 Db 262 TCCACCCGTCGATCAGAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGACAGATTTTC 321
 QY 324 ACCCTGGAATCACTAGAGTGAAGGCTGAGGATGAGGATGGGCTGTATTACTCTCAACAACCTT 383
 Db 322 ACCCTGGAATCACTAGAGTGAAGGCTGAGGATGAGGATGGGCTGTATTACTCTCAACAACCTT 381
 QY 384 GTAGAGTATCCATTCAGGTTCCGGCTCGGGGACAAAGTTGGAATAAAAA 431
 Db 382 GTAGAGTATCCGTCACATTCGGAGGGGGGACCAAGCTGGAATAAAAA 429
 RESULT 3
 AAQ12012
 ID AAQ12012 standard; DNA; 429 BP.
 AC AAQ12012;
 XX
 DT 19-AUG-1991 (first entry)
 XX
 DE Sequence encoding mouse Mab 2E12 L chain V region.
 XX
 KW HIV-1; chimera; ds.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..429
 FT /*tag= a
 XX
 XX WO9107494-A.
 XX
 PD 30-MAY-1991.
 XX
 PF 13-NOV-1990; 90WO-US06627.
 XX
 PR 13-NOV-1989; 89US-0433703.
 XX
 FA (XOMA-) XOMA CORP.
 XX
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 XX
 DR WPI; 1991-178106/24.
 DR P-PSDB; AARI2232.
 XX
 PT New chimeric mouse human antibodies - used in treatment, diagnosis
 PT and prophylaxis of HIV infections.
 XX
 PS Disclosure; Fig 1; 108pp; English.
 XX
 CC The mouse VL gene product may be used to produce chimeric mouse-
 CC human Abs against HIV-1 comprising human Ig constant regions and
 CC murine variable regions. These novel sequence are useful in
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be
 CC produced by a bacterial, yeast or mammalian expression system.
 XX
 SQ Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 other;
 Query Match 83.8%; Score 366.4; DB 12; Length 429;
 Best Local Similarity 93.6%; Pred. No. 1.7e-102;
 Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 QY 24 CAGGACCTCACCATCAGGATCTCTGTTCAGTTCTGGGGGTGCTATGTTCTGGATCTCT 83
 Db 22 CAAGTCTCAGAAATCAGGTGCTCTCTTCAGTTCTGGGGGTGCTATGTTCTGGATCTCT 81
 QY 84 GAGTCACTGGGGATATTGTGATATACCAGGATGACACTCTCCATCTCTGCTCACTCTGGA 143
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||

Db 82 GGAGTCAGTGGGAGATTCTGATAACCCAGGATGAATCTCCAACTCTGTCACTTCTGGA 141
 QY 144 GAATCAGTTCCATCTCCTGCAGGCTCTAGTAAGAGTCTCCTCTATAAGGATGGGAAGACA 203
 Db 142 GAATCAGTTCCATCTCCTGCAGGCTCTAGTAAGAGTCTCCTCTATAAGGATGGGAAGACA 201
 QY 204 TACTTGAATGGTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGATTTGATG 263
 Db 202 TACTTGAGTTGGTTCTGCAGAGACCAGGACAATCTCCGAGCTCCTGATCTATCTGATG 261
 QY 264 TCCACCCGTCGATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGACAGATTTTC 323
 Db 262 TCCACCCGTCGATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGACAGATTTTC 321
 QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGAGGATGGGCTGTATTACTCTCAACAACCTT 383
 Db 322 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGAGGATGGGCTGTATTACTCTCAACAACCTT 381
 QY 384 GTAGAGTATCCATTCAGGTTCCGGCTCGGGGACAAAGTTGGAATAAAAA 431
 Db 382 GTAGAGTATCCGTCACATTCGGAGGGGGGACCAAGCTGGAATAAAAA 429
 RESULT 4
 AAV09791
 ID AAV09791 standard; cDNA; 340 BP.
 XX
 AC AAV09791;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE DNA encoding the light chain of the catalytic antibody 3B9.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..340
 FT /*tag= a
 FT /*note= *no stop codon given*
 XX
 XX WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 XX WPI; 1998-077166/07.
 DR P-PSDB; AAW39801.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 PS Disclosure; Fig 17; 147pp; English.
 XX
 CC The present sequence encodes the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used

CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).

XX Sequence 340 BP; 86 A; 72 C; 88 G; 93 T; 1 other;

XX Query Match 72.6%; Score 317.2; DB 19; Length 340;
 XX Best Local Similarity 96.2%; Pred. No. 2e-87;
 XX Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGTAACCCAGGATGAATCTCCAATCCTGCTCACTTCTCGAGAAATCAGTTTCC 155
 DB 1 GATATTGTGATGACCCAGGATGAATCTCCAATCCTGCTCACTTCTCGAGAAATCAGTTTCC 60

QY 156 ATCTCCTGCAGGCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATATCTTGAATTGG 215
 DB 61 ATCTCCTGCAGGCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120

QY 216 TTCTCTCAGAGACAGACAACTCTCCTCAGCTCTCTGATGTATTGATGCCACCCGTGCA 275
 DB 121 TTCTCTCAGAGACAGACAACTCTCCTCAGCTCTCTGATGTATTGATGCCACCCGTGCA 180

QY 276 TCAGGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTCTCAGGCACAGATTTACCCCTGGAAATC 335
 DB 181 TCAGGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTCTCAGGCACAGATTTACCCCTGGAAATC 240

QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATCTGTCAACAACACTTGTAGAGTATCCA 395
 DB 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATCTGTCAACAACACTTGTAGAGTATCCA 300

QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAGC 433
 DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAGC 338

RESULT 5
 AAV09789
 ID AAV09789 standard; cDNA; 368 BP.
 XX
 AC AAV09789;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE DNA encoding the light chain of the catalytic antibody 2A10.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction; ss.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH CDS 1..339
 FT /*tag= a
 FT /note= "no stop codon given"
 XX

PN W09749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX P-PSDB; AAW39882.

XX New catalytic antibodies able to decompose cocaine, single-chain

PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

XX Disclosure: Fig 21; 147pp; English.

XX The present sequence encodes the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).

XX Sequence 368 BP; 95 A; 81 C; 94 G; 98 T; 0 other;

XX Query Match 72.6%; Score 317.2; DB 19; Length 368;
 XX Best Local Similarity 96.2%; Pred. No. 2.1e-87;
 XX Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGTAACCCAGGATGAATCTCCAATCCTGCTCACTTCTCGAGAAATCAGTTTCC 155
 DB 1 GATATTGTGATGACCCAGGATGAATCTCCAATCCTGCTCACTTCTCGAGAAATCAGTTTCC 60

QY 156 ATCTCCTGCAGGCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATATCTTGAATTGG 215
 DB 61 ATCTCCTGCAGGCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120

QY 216 TTCTCTCAGAGACAGACAACTCTCCTCAGCTCTCTGATGTATTGATGCCACCCGTGCA 275
 DB 121 TTCTCTCAGAGACAGACAACTCTCCTCAGCTCTCTGATGTATTGATGCCACCCGTGCA 180

QY 276 TCAGGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTCTCAGGCACAGATTTACCCCTGGAAATC 335
 DB 181 TCAGGAGTCTCAGACCCGTTTGTAGTGGCAGTGGGTCTCAGGCACAGATTTACCCCTGGAAATC 240

QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATCTGTCAACAACACTTGTAGAGTATCCA 395
 DB 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATCTGTCAACAACACTTGTAGAGTATCCA 300

QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAGC 433
 DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAGC 338

RESULT 6
 AAV09802
 ID AAV09802 standard; cDNA; 420 BP.

XX AAV09802;

XX 16-JUN-1998 (first entry)

DE DNA encoding the light chain of the catalytic antibody 12H1.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction; ss.

OS Mus sp.

XX Key Location/Qualifiers

XX CDS 53..391

XX /*tag= a

XX /note= "no stop codon given"

XX W09749800-A1.

XX 31-DEC-1997.

PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
DR P-PSDB; AAW39803.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Disclosure; Fig 23; 147pp; English.
XX
XX The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 420 BP; 98 A; 95 C; 115 G; 108 T; 4 other;

Query Match 72.3%; Score 316; DB 19; Length 420;
Best Local Similarity 95.6%; Pred. No. 5.1e-87;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTT 153
DB 51 GCGATATTGTGATGACGAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTT 110
QY 154 CCATCTCCTCGCAGGCTAGTAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT 213
DB 111 CCATCTCCTCGCAGGCTAGTAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT 170
QY 214 GGTTCCTCGAGACAGCAGACATCTCCTCAGCTCCTGATGATTTGATGCCACCGTG 273
DB 171 GGTTCCTCGAGACAGCAGACATCTCCTCAGCTCCTGATGATTTGATGCCACCGTG 230
QY 274 CATCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTCAACCTGGAAA 333
DB 231 CATCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTCAACCTGGAAA 290
QY 334 TCAGTAGAGTGAAGGCTGAGGATGGGGTGTGTTACTGTCAACAACCTGTAGAGTATC 393
DB 291 TCAGTAGAGTGAAGGCTGAGGATGGGGTGTGTTACTGTCAACAACCTTTGTAGACTATC 350
QY 394 CATTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 351 CATTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 390

RESULT 7
AAV09793
ID AAV09793 standard; cDNA; 368 BP.
XX
AC AAV09793;
XX
XX 18-JUN-1998 (first entry)
DT
XX DNA encoding the light chain of the catalytic antibody 6A12.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction; ss.

XX Mus sp.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..339
FT /*tag= a
FT /note= "no stop codon given"
XX
PN WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
DR P-PSDB; AAW39886.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Disclosure; Fig 19; 147pp; English.
XX
XX The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 368 BP; 95 A; 80 C; 93 G; 100 T; 0 other;

Query Match 70.8%; Score 309.2; DB 19; Length 368;
Best Local Similarity 94.7%; Pred. No. 6e-85;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTCTGATTAACCCAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTTCC 155
DB 1 GATATGGTGTAGACGCGAAGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTTCC 60
QY 156 ATCTCCTCGAGGCTAGTAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
DB 61 ATCTCCTCGAGGCTAGTAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
QY 216 TTCTCGAGAGCAGCAGACATCTCCTCAGCTCCTGATGATTTGATGTCACCCCGTGCA 275
DB 121 TTCTCGAGAGCAGCAGACATCTCCTCAGCTCCTGATGATTTGATGTCACCCCGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTCAACCTGGAAATC 335
DB 181 TCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTCAACCTGGAAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATGGGGTGTGTTACTGTCAACAACCTTTGTAGAGTATCCA 395
DB 241 AGTAGAGTGAAGGCTGAGGATGGGGTGTGTTACTGTCAACAACCTTTTGAAGACTATCCA 300
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

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XX WO9002569-A.
XX 22-MAR-1990.
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XX 06-SEP-1989; 89WO-US03852.
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XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX WPI; 1990-115825/15.
XX P-PSDB; AAR09420.
XX
XX Chimeric mouse-human antibodies - prepd. using genes coding for
XX constant human region murine variable region, esp. to 3 tumour
XX antigen
XX
XX Claim 13; Page 123 + Fig 7; 173pp; English.
XX
XX Shown is the nucleotide sequence from the end of the oligo-dC tail
XX to the Jk1-Ck junction. The sequence is used in the prodn. of a
XX chimeric antibody mol. comprising two light chains and two heavy chains,
XX each having a constant region (human) and a variable region (murine)
XX having specificity to an antigen bound by murine monoclonal antibody
XX (Mab) B38.1. The chimeric antibodies can be used for any purpose for
XX which the original murine Mabs can be used, with the advantage that
XX they are more compatible with the human body. They are esp. used for
XX the diagnosis and treatment of cancer.
XX
XX SQ Sequence 441 BP; 101 A; 106 C; 114 G; 120 T; 0 other;
XX
XX Query Match 63.4%; Score 277.2; DB 11; Length 441;
XX Best Local Similarity 79.8%; Pred. No. 4.3e-75;
XX Matches 327; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
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DB 28 CAAGTTCGAGAATGAGGTTCTCTGTCTCAGCTTCTGGGGTGTCTTGTCTGGATCCCT 87
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RESULT 12
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ID AAT43434 standard; CDNA; 441 BP.
XX
AC AAT43434;
XX
DT 12-FEB-1997 (first entry)
XX
DE Mab B38-1 light chain variable region CDNA.
XX
KW Chimeric antibody; monoclonal antibody; B38.1;
XX antibody engineering; tumour; antigen; breast carcinoma;
XX lung carcinoma; colon carcinoma; ovary carcinoma; cancer;
XX diagnosis; therapy; light chain; ss.
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XX
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PF 06-SEP-1988; 88US-0240624.
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PR 06-MAY-1991; 91US-0659401.
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XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX 27-DEC-1994; 94US-0364001.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX WPI; 1997-011249/01.
XX P-PSDB; AAW06209.
XX
XX Chimeric mouse-human antibodies - recognise a human tumour antigen,
XX used for the treatment and diagnosis of human cancers
XX
XX Example 3; Fig 7; 102pp; English.
XX
XX A CDNA clone (AAT43434) codes for the light chain variable region
XX (AAW06209) of mouse monoclonal antibody (Mab) B38-1, and extends from
XX the end of the oligo-dC tail to the J kappa-C kappa junction. It
XX was obt'd. from a B38-1 hybridoma CDNA library by screening with a
XX mouse C kappa region probe. Mab B38.1 (IgG1) binds to an antigen
XX that is expressed on the surface of human lung, breast, colon and
XX ovary carcinomas, but not on normal adult tissues. Light chain and
XX heavy chain variable region (see also AAT43435-43) sequences can be
XX used with human constant region sequences to express mouse-human
XX chimeric antibodies in transformed host cells. The antibodies have
XX specificity to human tumour antigens and can be used for the
XX treatment and diagnosis of human cancer.
XX
XX SQ Sequence 441 BP; 101 A; 106 C; 114 G; 120 T; 0 other;
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XX Query Match 63.4%; Score 277.2; DB 18; Length 441;
XX Best Local Similarity 79.8%; Pred. No. 4.3e-75;
XX Matches 327; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
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PF 24-SEP-1992; 92EP-0308680.
XX
PR 26-SEP-1991; 91GB-0020467.
XX
PA (CLLT ) CELLTECH LTD.
XX
PI Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;
PI Menendez AT, Owens RJ;
XX
DR WPI; 1993-102837/13.
DR P-PSDB; AAR33951.
XX
XX Anti-human milk fat globule humanised antibodies - useful as
PT conjugate for in-vivo diagnosis and therapy of e.g. ovarian or
PT breast cancer
XX
PS Disclosure; Page 19-20; 57pp; English.
XX
CC The sequences given in AAQ38877-78 encodes the heavy and light chain
CC variable domains of CTM01 respectively. These sequences were isolated
CC by PCR using the primer sequences given in AAQ38879-80. Examination of
CC the derived amino acid sequences from these sequences revealed
CC considerable homology with other characterised immunoglobulin genes.
CC The murine monoclonal antibody (MAB), CTM01, was confirmed to be an
CC IgG-kappa antibody. CTM01 was used in the production of a humanised
CC antibody for in vivo diagnosis and therapy of carcinomas of ovary,
CC breast, uterus and lung.
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Query Match 53.2%; Score 276.4; DB 14; Length 399;
Best Local Similarity 80.9%; Pred. No. 7.3e-75;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 96 GATATTGTATACCCAGGATGAACCTCCAAATCCTGTCCTGATGTTGATGTCAGTATTC 155
DB 61 GATATTGTATGACTCAGGCTGACCCCTCTGTTCTGTCACCTCTGGAGATCATTTGCC 120

QY 156 ATCTCTGCAGGCTAGTAGAGTCTCCTGTATAAGGATGGGAAGACATCTGAATTGG 215
DB 121 ATTTCTGCAGGCTAGTAGAGTCTCCTGTATAAGGATGGGAAGACATCTGAATTGG 180

QY 216 TTTCTGCAGACGAGGACAAATCTCTCAGCTCCTGATGTTATTTGATGCCACCGTGCA 275
DB 181 TTCTCTGCAGAGGCCAGGCCAGTCTCCTCAACTCCTGATATATCGGATGTCCAACCTTGC 240

QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTCAAGGCACAGATTTCACCTGGAAATC 335
DB 241 TCCGGAGTCCACAGACAGGTTTCAGTGGCAGTGGGTCAAGAACTGCTTTCACACTGAGAGTC 300

QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
DB 301 AGTAGAGTGGAGGCTGAGGATGGGTGTTTATCTGTATGCAACATCTAGAATATCTCT 360

QY 396 TTCACGTTCGGCTCGGGGCAAAAGTTGGAATAAAACG 433
DB 361 TTCACGTTCGGTCTGGGACCAAGCTGGAGCTGAACG 398

RESULT 15
ID AAT85855
XX AAT85855 standard; cDNA; 399 BP.
XX
AC AAT85855;
XX
XX 14-JAN-1998 (first entry)
XX
XX Anti-HMEG MAB CTM01 light chain variable region cDNA.
XX
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KW Humanised antibody; CDR-grafted antibody; chimeric antibody; CTM01;
KW complementarity determining region; human milk fat globule; HMEG;
KW monoclonal antibody; MAB; mouse; cancer; breast cancer;
KW ovary carcinoma; lung cancer; uterus cancer; diagnosis; therapy;
KW ss.
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OS Mus musculus.
XX
XX Key Location/Qualifiers
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PN EP781845-A2.
XX
XX 02-JUL-1997.
PD
XX
PF 24-SEP-1992; 92EP-0308680.
XX
PR 26-SEP-1991; 91GB-0020467.
XX
XX (CLLT ) CELLTECH THERAPEUTICS LTD.
XX
XX Adair JR, Baker TS, Hamann PR, Hinman LM, Lyons AH;
XX Menendez AT, Owens RJ;
XX
XX WPI; 1997-334902/31.
XX P-PSDB; AAW29751.
XX
XX DNA encoding composite heavy and light chains of humanised antibody
XX - specific for human milk fat globule, useful in cancer diagnosis or
XX therapy
XX
PS Claim 4; Page 19-20; 53pp; English.
XX
XX This cDNA sequence comprises a coding sequence for the light chain
XX variable region VL (see AAW29751) of murine anti-human milk fat
XX globule (HMEG) monoclonal antibody CTM01. It was isolated from
XX CTM01 hybridoma cDNA using a light chain constant region probe.
XX CTM01 VL and VH (see AAT85854) nucleic acids can be used in the
XX construction of recombinant chimeric humanised antibodies and
XX recombinant CDR-grafted humanised anti-HMEG antibodies. These may
XX be conjugated with labels or drugs (especially methyltrithio
XX antitumour agents) and used for diagnosis or therapy of human
XX carcinomas, e.g. of the ovary, breast, uterus and lung.
XX
SQ Sequence 399 BP; 80 A; 95 C; 111 G; 113 T; 0 other;
```

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Query Match 63.2%; Score 276.4; DB 18; Length 399;
Best Local Similarity 80.9%; Pred. No. 7.3e-75;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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QY 36 ATGAGGTTCTCTGTTACAGTTCTGGGGGCTGTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 ATGAGGTGCCCTAGCTGAGTTCCTGGGGGCTGTTGCTCTGGATCCTCGGCCATTTGGG 60

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAAATCTCTGTCACCTCTGGAGAATCAGTTTCC 155
DB 61 GATATTGTGATGACTCAGGCTGACCCCTCTGTTCTGTCACCTCTGGAGATCATTTATCC 120

QY 156 ATCTCTCTCAGGCTCAGTAAGAGTCTCCTGTATAGGATGGGAAGACATCTGAATTGG 215
DB 121 ATTTCTCTCAGGCTCAGTAAGAGTCTCCTGTATAGTATATGCGACACTTCTTCTGATTGG 180

QY 216 TTTCTGCAGACGAGGACAAATCTCTCAGCTCCTGATGTTATTTGATGCCACCGTGCA 275
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 42.2347 Seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagcttaccagttactcagc.....agttggaaataaaacgtacg 437

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	247	56.5	968	9	US-09-924-340-7
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3	245.2	56.1	738	9	US-10-158-646-61
4	241.2	55.2	954	9	US-09-479-614-19
5	241.2	55.2	954	9	US-09-479-614-21
6	238.4	54.6	726	9	US-09-479-614-23
7	238.4	54.6	726	9	US-09-479-614-24
8	223.6	51.2	399	10	US-09-905-243-55
9	222.8	51.0	2272	9	US-10-158-646-63
10	220.4	50.4	413	10	US-09-748-960-7
11	218.6	50.0	420	9	US-09-341-894-3
12	217.4	49.7	492	9	US-10-060-036-3613
13	214	49.0	420	10	US-09-881-823-9
14	211.6	48.4	720	9	US-10-124-905-5
15	211.6	48.4	720	9	US-09-948-429B-5
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17	210.8	48.2	723	9	US-09-988-115A-60
18	210.4	48.1	396	10	US-09-748-960-1
19	208.6	47.7	729	12	US-10-006-773-10
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					Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-924-340-7

; Sequence 7, Application US/09924340

; Publication No. US20030027248A1

; GENERAL INFORMATION:

; APPLICANT: Bejanin, Stephanie

; APPLICANT: Tanaka, Hiroaki

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

; FILE REFERENCE: 91.US2.REG

; CURRENT APPLICATION NUMBER: US/09/924,340

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: JPatent

; SEQ ID NO 7

; LENGTH: 968

; TYPE: DNA

; ORGANISM: Homo sapiens

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; NAME/KEY: CDS

; LOCATION: 32..748

; NAME/KEY: 3'UTR

; LOCATION: 749..968

; NAME/KEY: polyA.signal

; LOCATION: 928..933

; NAME/KEY: polyA.site

; LOCATION: 953..968

US-09-924-340-7

Query Match

Best Local Similarity

Matches 307; Conservative

Score 247; DB 9; Length 968;

Pred. No. 1.6e-73;

Mismatches 100; Indels

0; Gaps

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37 193.2 44.2
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QY 90 AGTGGGATATTGATGAACCCAGGATGAACCTCCCAATCTGTCACCTCTGAGATCA 149
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RESULT 2

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US-09-992-600A-7
; Sequence 7, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91 US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Jpatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..748
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; FEATURE:
; NAME/KEY: polyA_signal
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US-09-992-600A-7

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Query Match 56.5%; Score 247; DB 9; Length 968;
Best Local Similarity 75.4%; Pred. No. 1.6e-73;
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QY 390 TATCCATTCAGTTCGCTCGGGACAAAGTTGGAATAAAACGTAC 436
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RESULT 3

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US-10-158-646-61
; Sequence 61, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20030073105A1 1329931.2
US-10-158-646-61
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Query Match 56.1%; Score 245.2; DB 9; Length 738;
Best Local Similarity 76.6%; Pred. No. 5.7e-73;
Matches 314; Conservative 0; Mismatches 93; Indels 3; Gaps 1;
QY 30 CTCACATGAGGTTCTCTGTTTCAGTCTTTCTGGGGGTGCTTATGTTCTGATCTCTGGAGTC 89
Db 15 CTCACATGAGGCTCCCTGCTCAGCTCCTGGGCTGCTAATGCTCTGGGTCCTGGGTCC 74
QY 90 AGTGGGATATTGATGAACCCAGGATGAACCTCCCAATCTCTGATGTTCTGAGATCA 149
Db 75 AGTGGGATATTGATGACCCAGACTCCAGCTCCCTGCCCGTCACCCCTGGAGAGCG 134
QY 150 GTTTCATCTCTCGAGGTTCTAGTAAGAGTCTCTGTTATA--AGGATGGGAAGACATAC 206
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[illegible]

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; SEQ ID NO 23
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-23

Query Match      54.6%; Score 238.4; DB 9; Length 726;
Best Local Similarity 74.8%; Pred. No. 1.2e-70;
Matches 299; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGAGGTTCCCTGCTCAGCTCTGGAGTCAATGCTCTGGATCCCAAGGATCAGTGGG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 96 GATATTGTGATTAACCCAGGATGAATCTTCCAAATCCTGTCATCTCTGGAGATCAGTTTCC 155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GATATTGTGATGAGCAGACCCCTCTGTCCTGCTCCGTCACCCCTGGAGAGCCAGCCTCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 156 ATCTCCTGCAAGTCTAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATCTTGAATTGG 215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATCTCCTGCAAGGCTAGTACAGCTCTGCTGTACAGTGATGGAATCTTCTGAATTGG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 216 TTCTGTCAGACAGCAGCAATCTCTCAGCTCCTGAGTGATTTGATCTCCACCCGTGCA 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TACCTGTCAGAGCAGGCGGCTCCACGCGCTTGTATCTATCTTTTCCAAACCGGGAC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 276 TCAGGAGTCTCAGACCCGTTTCTAGTGGTCTAGGTCAGGACAGATTTCCACCTGGAATC 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TCTGGGTCCCAGACAGATTTCCAGGCGTCTCCAGCGCTTGTATCTTTTCCAAACCGGGAC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGCAGGTTGGAGGCTGACGAGCTCGGTGTTTATTCTCGGTCAAGGTTTACAGCATCCT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 396 TTCACGTTTCGGCTCGGGGACAAAAGTTTGGAAATAAAGCTA 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CTCACCTTTCCGCCCCAGGTACCAAGCTGGAGATCAAAACGGA 400
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RESULT 7
US-09-479-614-24/c
; Sequence 24, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-24
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Db 606 ATCTCTGTCAGGCGCACTCAGAGCCTCCTGTACAGTGATGGAAATCTATCTGAAATGG 547
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Qy 216 TTCTGTCAGACAGCAGCAATCTCTCAGCTCCTGATGATGATGATGATGATGATGATGATGATG 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 TACCTGTCAGAGCAGGCGGCTCTCCACGCGCTTGTATCTTTTCCAAACCGGGAC 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 276 TCAGGAGTCTCAGACCCGTTTCTAGTGGTCTAGGTCAGGACAGATTTCCACCTGGAATC 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 TCTGGGTCCCAGACAGATTTCCAGGCGTCTCCAGGCGTCTCCAGGCGTCTCCAGGCGTCT 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 AGCAGGTTGGAGGCTGACGAGCTCGGTGTTTATTCTCGGTCAAGGTTTACAGCATCCT 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 396 TTCACGTTTCGGCTCGGGGACAAAAGTTTGGAAATAAAGCTA 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 CTCACCTTTCCGCCCCAGGTACCAAGCTGGAGATCAAAACGGA 327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-09-905-243-55
; Sequence 55, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(399)
US-09-905-243-55

Query Match      51.2%; Score 223.6; DB 10; Length 399;
Best Local Similarity 72.6%; Pred. No. 9.4e-66;
Matches 289; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTTATGTTCTGATCTCTGGAGTCAGTGGG 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATGAGGTTCCCTGCTCAGCTCTCCGCGCTGCTATGCTCTGCGTCCCGGATCCAGTGGG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 96 GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCATCTCTGGAGATCAGTTTCC 155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GATATTGTGATGATCAGTCTCCACTCTCCCTGCGCTCTCCCTGGAGACGCCCTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 156 ATCTCCTGCAAGTCTAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATCTTGAATTGG 215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATCTCCTGCAAGGCTAGTACAGCTCTTGTACATGATGATGATGATGATGATGATGATGATG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 216 TTCTGTCAGACAGCAGCAATCTCTCAGCTCCTGATGATGATGATGATGATGATGATGATGATG 275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TTACAACAGAGCAGGCGGCTCCAAACCTCTCCAGACTCTGATGATGATGATGATGATGATG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 276 TCAGGAGTCTCAGACCCGTTTCTAGTGGTCTAGGTCAGGACAGATTTCCACCTGGAATC 335
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TCTGGGTCCCAGACAGATTTCCAGGCGTCTCCAGGCGTCTCCAGGCGTCTCCAGGCGTCT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGCAGGTTGGAGGCTGAGGATGTTGGGTGTTTATTCTCGGTCAAGGTTTACAGCATCCT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 396 TTCACGTTTCGGCTCGGGGACAAAAGTTTGGAAATAAAGCTA 433
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QY 212 TTGGTTCTGCAGACAGCAGGACAAATCTCTCAGCTCCTCATGTATTTGATGTCACCCG 271
Db 189 TTGGTTGTACAGAGGCGCAGCCAGTCTCCAAAGCGCCTAATCTATCTGTGTCTAAACT 248
QY 272 TGCATCAGGAGCTCTCAGACCGGTTTACTGGCAGTGGGTGAGGACAGATTTACCCCTGGA 331
Db 249 GGACTCTGGAGTCCTCAGAGGTTCACTGGCAGTGGATCAGGACAGATTTCACTGAA 308
QY 332 AATCAGTAGAGTGAAGCTGAGGATGTTGGGTGTGTATTTACTGTCAACAACATTTGAGAGTA 391
Db 309 AATCAGCAGAGTGAGGCTGAGGATTTGGGAGTTTATTTGCTGGCAAGGTACACATTT 368
QY 392 TCCATTACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGTACG 437
Db 369 TCCGCTCAGTTCGGTGTGGGACCAAGCTGGAGCTGAAACGTAAG 414

RESULT 14
US-10-124-905-5
; Sequence 5, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124.905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..720
US-10-124-905-5

Query Match

48.4%; Score 211.6; DB 9; Length 720;

Best Local Similarity 70.4%; Pred. No. 1.4e-61;
Matches 283; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTCCTGGGGGTGCTTATGTTCTGTGATCTCTGGAGTCACTGGG 95
Db 1 ATGAGGCTCCCTGCTCAGCTCCTCGGGGTGCTTATGTTCTGTGCTCCCGGTCCAGTGGG 60
QY 96 GATATTGTATACCCAGGATGAACCTCTCCAATCCTGTCACCTCTGGAGATCACTTTCC 155
Db 61 GAAGTTGTGATGACTCAGTCTCAGTCTCCCTTCCATCAACCTGGAGAGCCGCTCC 120
QY 156 ATCTCTCAGGTTCTAGTAAGAGTCTCTCTGATAAGGATGGGAAGACATCTTGAATGG 215
Db 121 ATCTCTGTTAGTCTAGTCAAGCCCTTAAACACAGTAATGGAGACACCTTCTGAGTTGG 180
QY 216 TTCTCTCAGAGACAGGACAACTCTCTCAGCTCCTGATGATTTGATGTCACCTGCA 275
Db 181 TATCAGCAGAAGCCAGGCCAAGCTCCAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC 240
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTACCTGGAAATC 335
Db 241 TCTGGGTCTCCAGACAGATTCAGCGCAGTGGGCGAGGACAGATTTACACTGAAATC 300
QY 336 ACTAGATGAAGCTCAGGATGTTGGGTGTATTTACTGTCAACAACCTTTGATAGATATCA 395
Db 301 AGCGCAGTGGAGCTCAAGATGTTGGGTGTTTATTTCTGGGGCAAGGTACAAGGACTCCT 360
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGTACG 437
Db 361 CCACCTTCGGGAGGAGGACCAAGGTGGAAATCAAAACGTACG 402

RESULT 15
US-09-948-429B-5
; Sequence 5, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..720
US-09-948-429B-5

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; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..720
US-09-948-429B-5

Query Match      48.4%; Score 211.6; DB 9; Length 720;
Best Local Similarity 70.4%; Pred. No. 1.4e-61;
Matches 283; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db 1 ATGAGCCTCCCTGTCTCAGCTCCTCGGGTCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60

Qy 96 GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 61 GAAATTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGCCCGCCCTCC 120

Qy 156 ATCTCTGCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATACTTGAATTGG 215
Db 121 ATCTCTGTAGTCTAGTCAAGGCTTAAACACAGTAATGGAGACACCTTCTCTGAGTTGG 180

Qy 216 TTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
Db 181 TATCAGCAGAGCCAGGCCAACCTCCRAGGCTCCTGATTTATAAGGTTTCTAACCCGGAC 240

Qy 276 TCAGAGTCTCAGACCCGTTTGTAGTGGAGTGGGTGAGCAGACAGATTTACCCCTGGAATC 335
Db 241 TCTGGGTCCAGACAGATTCAGGGGAGTGGGGCAGGACAGATTTACACTGAAATC 300

Qy 336 AGTAGAGTGAAGGCTGAGAGTGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 395
Db 301 AGCCAGTGGAGGCTGAAGATGTGGGTTTATTTCTCGGGCAAGGTACAAGGACTCCT 360

Qy 396 TTCAGTTTCGGCTCGGGACAAAGTTGGAATAAAACGTACG 437
Db 361 CCCACTTTCGGCGGAGGACCAGGTGGAATCAAACGTACG 402
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Search completed: April 26, 2003, 09:24:09
Job time : 47.2347 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 18,1006 seconds
(without alignments)
7404,053 Million cell updates/sec

Title: US-09-674-716B-2
Perfect score: 437
Sequence: 1 agctttacagttactcagc.....agttggaataaagcagtcag 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.2	72.6	339	2	US-08-672-345C-88
2	317.2	72.6	339	4	US-09-214-095D-99
3	317.2	72.6	368	2	US-08-672-345C-86
4	317.2	72.6	368	4	US-09-214-095D-107
5	316	72.3	420	4	US-09-214-095D-111
6	309.2	70.8	368	2	US-08-672-345C-90
7	309.2	70.8	368	4	US-09-214-095D-103
8	293.2	67.1	464	1	US-08-438-123-15
9	276.4	63.2	399	1	US-08-253-877C-9
10	276.4	63.2	399	2	US-08-452-164A-9
11	276.4	63.2	399	3	US-08-603-024-3
12	249.6	57.1	336	3	US-08-483-749A-3
13	248.4	56.8	339	4	US-09-406-532-13
14	240	54.9	882	1	US-08-392-419-3
15	236	54.0	373	3	US-08-732-708C-40
16	230.8	52.8	1095	3	US-08-875-811-52
17	230.8	52.8	1098	3	US-08-875-811-54
18	226.2	51.8	405	1	US-08-259-372A-11
19	226.2	51.8	405	1	US-08-468-671-11
20	223.6	51.2	427	1	US-08-053-171-8
21	221.4	50.7	325	1	US-08-468-661-4
22	221.4	50.7	325	1	US-08-466-272A-4
23	221.4	50.7	325	1	US-08-478-857-4
24	221.4	50.7	325	2	US-08-471-771-4
25	221.4	50.7	325	3	US-09-130-783-4
26	219	50.1	434	1	US-08-053-171-4
27	212.8	48.7	394	1	US-08-129-930B-93

28	212.8	48.7	394	4	US-08-134-346A-48	Sequence 48, Appl
29	212.8	48.7	394	4	US-08-976-288A-93	Sequence 93, Appl
30	211.6	48.4	720	3	US-08-487-550-5	Sequence 5, Appl
31	211.2	48.3	394	1	US-07-977-696C-64	Sequence 64, Appl
32	211.2	48.3	394	1	US-08-129-930B-64	Sequence 64, Appl
33	211.2	48.3	394	4	US-08-976-288A-64	Sequence 64, Appl
34	206.6	47.3	424	3	US-08-589-939-8	Sequence 8, Appl
35	206.6	47.3	537	5	PCT-US91-02942-2	Sequence 2, Appl
36	206.6	47.3	537	5	PCT-US91-02946-2	Sequence 2, Appl
37	206.4	47.2	394	1	US-07-977-696C-26	Sequence 26, Appl
38	206.4	47.2	394	1	US-08-129-930B-26	Sequence 26, Appl
39	206.4	47.2	394	4	US-08-134-346A-13	Sequence 13, Appl
40	206.4	47.2	394	4	US-08-976-288A-26	Sequence 26, Appl
41	206.2	47.2	339	1	US-08-264-093-9	Sequence 9, Appl
42	205.8	47.1	714	3	US-09-192-545-3	Sequence 3, Appl
43	205	46.9	384	1	US-08-482-882-44	Sequence 44, Appl
44	205	46.9	384	1	US-08-483-389-44	Sequence 44, Appl
45	205	46.9	384	2	US-08-487-113D-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-88
; Sequence 88, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-672-345C-88

Query Match 72.6%; Score 317.2; DB 2; Length 339;
Best Local Similarity 96.2%; Pred. No. 7.8e-97;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 96 GATATTGTGTAACCCAGGATGAACCTCCAACTCTCTGAGAAATCAGTTTCC 155
|||||
Db 1 GATATTGTGATGACCCAGGATGAACCTCCAACTCTCTGAGAAATCAGTTTCC 60
Qy 156 ATCTCTTCAGGCTTAGTAAGAGTCTCTGTATAGAGTGGAGACATACATCTGAATTGG 215
|||||

Db 61 ATCTCTCGAGGCTAGTAGGAGTCTCTCTATATAGGAGTGGGAAGACATCTTGAATTGG 120
QY 216 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGAGACAGGACAGATCTCTCAACTCTGATCTATTGATGTCACCCGTTC 180
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGCACAGATTTACCCCTGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGAACAGATTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 300
QY 396 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 2

US-09-214-095D-99
; Sequence 99, Application US/09214095D
; Patent No. 6280987

; GENERAL INFORMATION:
; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214, 095D
; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 99
; LENGTH: 339

; TYPE: DNA

; ORGANISM: Murline
US-09-214-095D-99

Query Match 72.6%; Score 317.2; DB 4; Length 339;
Best Local Similarity 96.2%; Pred. No. 7.8e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAATCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACCAAGACAGAACTCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
Db 61 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
QY 216 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGAGACAGGACAGATCTCTCAACTCTGATCTATTGATGTCACCCGTTC 180
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGCACAGATTTACCCCTGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGAACAGATTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 300
QY 396 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 3

US-08-672-345C-86

; Sequence 86, Application US/08672345C
; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 86:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 368 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-672-345C-86

Query Match 72.6%; Score 317.2; DB 2; Length 368;
Best Local Similarity 96.2%; Pred. No. 8.1e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAATCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACCAAGACAGAACTCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
Db 61 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
QY 216 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGAGACAGGACAAATCTCTCAGCTCCTGATCTATTTGATGTCACCCGTGCA 180
QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGCACAGATTTACCCCTGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGAACAGATTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGATATCCA 300
QY 396 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 4

US-09-214-095D-107
; Sequence 107, Application US/09214095D
; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214, 095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-107

Query Match          72.6%; Score 317.2; DB 4; Length 368;
Best Local Similarity 96.2%; Pred. No. 8.le-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTTC 155
DB 1 GATATGGTGATGACGCAAGACAACTCTCCAATCCTGTCACTTCTGGAGAAATCAGTTTC 60

QY 156 ATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATTGG 215
DB 61 ATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATTGG 120

QY 216 TTCTCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 275
DB 121 TTCTCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 180

QY 276 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAATC 335
DB 181 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAATC 240

QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACTGTAGAGATATCCA 395
DB 241 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACTGTAGAGATATCCA 300

QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 301 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 5
US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE OF INVENTION: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214.095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: V_segment
; LOCATION: (1)..(403)
; OTHER INFORMATION: n at any position represents any nucleotide including c,g,t,a,u
US-09-214-095D-111

Query Match          72.3%; Score 316; DB 4; Length 420;
Best Local Similarity 95.6%; Pred. No. 2.2e-96;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTT 153
DB 51 GCGATATGGTGATGACGCAAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTT 110

QY 154 CCATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATT 213
DB 111 CCATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATT 170

QY 214 GGTTCCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTG 273
DB 171 GGTTCCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTG 230
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QY 274 CATCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAA 333
DB 231 CATCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAA 290

QY 334 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACTGTAGAGATATC 393
DB 291 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACTTTGTAGACTATC 350

QY 394 CATTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 351 CATTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 390

RESULT 6
US-08-672-345C-90
; Sequence 90, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-672-345C-90
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Query Match          70.8%; Score 309.2; DB 2; Length 368;
Best Local Similarity 94.7%; Pred. No. 3.9e-94;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTTC 155
DB 1 GATATGGTGATGACGCAAGGATGAACCTCCCAATCCTGTCACTTCTGGAGAAATCAGTTTC 60

QY 156 ATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATTGG 215
DB 61 ATCTCCCTGCAGGCTAGTAGAGTCTCCTCTGATAAGGATGGGAGACATATCTTGAATTGG 120

QY 216 TTCTCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 275
DB 121 TTCTCTGCAGACAGGACAACTCCTCAGCTCCTGATGATTTGATGTCCACCCGTGCA 180

QY 276 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAATC 335
DB 181 TCAGGAGTCTCAGACCCGGTTTAGTGGCAGTGGGTGCGGACAGATTTCAACCTGGAAATC 240
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QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 301 TTCACGTTCCGGCTCGGGGACAAATTTGGAGATAAAACG 338

RESULT 7

US-09-214-095D-103
; Sequence 103, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 368
; TYPE: DNA
; ORGANISM: MURINE
US-09-214-095D-103

Query Match 70.8%; Score 309.2; DB 4; Length 368;
Best Local Similarity 94.7%; Pred. No. 3.9e-94;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTGACATCTCTGGAGAATCAGTTTCC 155
Db 1 GATATGTTGATGACGCAAGATGAACCTCTCCAATCCTGTGACATCTCTGGAGAATCAGTTTCC 60
QY 156 ATCTCTGCAGTCTAGTAGAGTCTCCGTATATAGGATGGGAACATACCTTGAATGG 215
Db 61 ATCTCTGCAGTCTAGTAGAGTCTCCGTATATAGGATGGGAACATACCTTGAATGG 120
QY 216 TTTCTGCAGAGACGAGCAAAATCTCTCAGCTCCTGATGATTTGATGTCCACCCGTCGA 275
Db 121 TTTCTGCAGAGACGAGCAAAATCTCTCAGCTCCTGATCTATTGATGTCCACCCGTCGA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACAGATTTTCAACCTGGAATC 240
QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 301 TTCACGTTCCGGCTCGGGGACAAATTTGGAGATAAAACG 338

RESULT 8

US-08-438-123-15
; Sequence 15, Application US/08438123
; Patent No. 5532293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 149-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-438-123-15

Query Match 67.1%; Score 293.2; DB 1; Length 464;

Best Local Similarity 82.2%; Pred. No. 1e-88;

Matches 337; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCAGAGGTTCTCTGTTCAGTTTCTGGGGGTCTTATGTTCTGGATCTCT 83
Db 30 CAAGTTCTCAGAATGAGTGCCTAGTCTGAGTTCCTCGGGCTCTCTGCTCTGGATCCT 89
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTTCTGGA 143
Db 90 GGAGTCAGTGGGGATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCACTCTGGA 149
QY 144 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTGATAAGGATGGGAAGACA 203
Db 150 GAGTCAGTATCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTGATAAGTGGCAACACT 209
QY 204 TACTTCAATTTGGTTTCTGCGAGACCCAGGACAAATCTCTCAGCTCCTGATGATTTGATG 263
Db 210 TACTTGTATTGTTCTCTGCGAGGCTCTCTCAGCTCCTGATGATATATCGGATG 269
QY 264 TCACCCGCTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTC 323
Db 270 TCCAACTTTGTTCTCAGGAGTCCCGACAGACAGGTTTCACTGGGCTGAGGACCTGCTTTC 329
QY 324 ACCTCGAATCAGTACGAGGCTGAGGATGTTAGTGGCAGTGGGTGAGGACAGATTTTC 383
Db 330 ACATGAGATCAGTAGAGTGGAGGCTGAGGATGTTAGTGGGTTTATTCTGCTGCAACACT 389
QY 384 GTAGAGTATCCATTTCACTGCTCGGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 390 CTAGAGTATCCGTTTCACTGCTCGGCTCTCGGGACCAAGCTGGAGCTGAAACG 439

RESULT 9

US-08-253-877C-9
; Sequence 9, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:

; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylnitro Antitumor
; Agents and Intermediates for Their Synthesis

```
;
;
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
;
; US-08-253-877C-9
;
; Query Match 63.2%; Score 276.4; DB 1; Length 399;
; Best Local Similarity 80.9%; Pred. No. 4e-83;
; Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
;
QY 36 ATGAGTTCTCTGTCAGTTTCTGGGGTGCCTATGTTCTGATCTCTGGAGTCAGTGGG 95
Db 1 ATGAGTGCCTAGCTAGTTCTGGGGTGCCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60
QY 96 GATATTGTGATAACCCAGGATGAACCTCCATCTGTCACCTCTGGAGAAATCAGTTTCC 155
Db 61 GATATTGTGATGACTCAGGCTGCACCCCTCTCTCTGTCACCTCTCTGGAGAGTCATTATCC 120
QY 156 ATCTCTCGAGGCTCTAGTAAAGTCTCTCTGATAGATGAGTGGGAGACATATCTGAATTGG 215
Db 121 ATTTCTCGAGGCTCTAGTAAAGTCTCTCTGATAGTGGGAGTCTCTTCTGTTATGG 180
QY 216 TTCTCGAGAGCAGGACAACTCTCTCAGCTCCTGATGATATTTGATCTCCACCCGTGCA 275
Db 181 TTCTCGAGAGCAGGACGAGTCTCTCTCACTCTGATATATCGGATGTCACACTTGGC 240
QY 276 TCAGGAGTCTCAGACCGTTTAGTGGCAGTGGGTGAGGACACAGATTTACCCCTGGAATC 335
Db 241 TCCGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGTGGGTCAGGAACTGCTTTTCCACTGAGAGTC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 395
Db 301 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 360
;
; RESULT 10
; US-08-452-164A-9
; Sequence 9, Application US/08452164A
; Patent No. 5877296
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;
;
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
;
; US-08-452-164A-9
;
; Query Match 63.2%; Score 276.4; DB 2; Length 399;
; Best Local Similarity 80.9%; Pred. No. 4e-83;
; Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
;
QY 36 ATGAGTTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGATCTCTGGAGTCAGTGGG 95
Db 1 ATGAGTGCCTAGCTAGTTCTGGGGTGCCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60
QY 96 GATATTGTGATAACCCAGGATGAACCTCCATCTGTCACCTCTCTGGAGAAATCAGTTTCC 155
Db 61 GATATTGTGATGACTCAGGCTGCACCCCTCTCTCTGTCACCTCTCTGGAGAGTCATTATCC 120
QY 156 ATCTCTCGAGGCTCTAGTAAAGTCTCTCTGATAGATGAGTGGGAGACATATCTGAATTGG 215
Db 121 ATTTCTCGAGGCTCTAGTAAAGTCTCTCTGATAGTGGGAGTCTCTTCTGTTATGG 180
QY 216 TTCTCGAGAGCAGGACAACTCTCTCAGCTCCTGATGATATTTGATCTCCACCCGTGCA 275
Db 181 TTCTCGAGAGCAGGACGAGTCTCTCTCACTCTGATATATCGGATGTCACACTTGGC 240
QY 276 TCAGGAGTCTCAGACCGTTTAGTGGCAGTGGGTGAGGACACAGATTTACCCCTGGAATC 335
Db 241 TCCGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGTGGGTCAGGAACTGCTTTTCCACTGAGAGTC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 395
Db 301 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 360
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QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
|||||
Db 361 TTCAGTTCCGTCGTGGGACCAAGCTGGAGCTGAAACG 398
|||||
RESULT 11
US-08-603-024-3
; Sequence 3, Application US/08603024
; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
; US-08-603-024-3

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Best Local Similarity 80.9%; Pred. No. 4e-83;
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QY 336 AGTAGAGTGAAGGCTCAGGATGTGGGTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
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RESULT 12
US-08-483-749A-3
; Sequence 3, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; US-08-483-749A-3

Query Match 57.1%; Score 249.6; DB 3; Length 336;
Best Local Similarity 83.9%; Pred. No. 3.5e-74;
Matches 282; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTCAGGCGACAGATTTCACCCCTGGAATC 335
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 694.49 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	348	100.0	348	6	AX010614	AX010614 Sequence
c	348	100.0	348	6	AX010645	AX010645 Sequence
3	292	83.9	740	6	AX076853	AX076853 Sequence
c	292	83.9	740	6	AX076855	AX076855 Sequence
5	277.6	79.8	410	9	HSIGKLV46	X72467 H.sapiens m
6	276	79.3	353	9	HSI272080	AJ272080 Homo sapi
7	276	79.3	360	9	HSTOP003	X93771 H.sapiens m
8	276	79.3	360	9	HSTOP016	X93774 H.sapiens m
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10	276	79.3	360	9	HSTOP220	X93792 H.sapiens m
11	276	79.3	360	9	HSTOP305	X93805 H.sapiens m
12	276	79.3	360	9	HSTOP307	X93807 H.sapiens m
13	276	79.3	377	9	HSIGKLV45	X72466 H.sapiens m
14	276	79.3	407	9	HSIGKLV31	X72452 H.sapiens m
15	274.4	78.9	360	9	HSTOP014	X93772 H.sapiens m
16	274.4	78.9	360	9	HSTOP027	X93778 H.sapiens m
17	274.4	78.9	360	9	HSTOP101	X93780 H.sapiens m
18	274.4	78.9	360	9	HSTOP103	X93782 H.sapiens m
19	274.4	78.9	360	9	HSTOP104	X93783 H.sapiens m
20	274.4	78.9	360	9	HSTOP204	X93785 H.sapiens m
21	274.4	78.9	360	9	HSTOP214	X93789 H.sapiens m
22	274.4	78.9	360	9	HSTOP217	X93790 H.sapiens m
23	274.4	78.9	360	9	HSTOP237	X93793 H.sapiens m
24	274.4	78.9	360	9	HSTOP243	X93796 H.sapiens m
26	274.4	78.9	360	9	HSTOP247	X93797 H.sapiens m
27	274.4	78.9	360	9	HSTOP254	X93799 H.sapiens m
28	274.4	78.9	360	9	HSTOP301	X93800 H.sapiens m
29	274.4	78.9	360	9	HSTOP303	X93802 H.sapiens m
30	274.4	78.9	360	9	HSTOP306	X93803 H.sapiens m
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35	272.8	78.4	360	9	HSTOP001	E35205 Human monoc
36	272.8	78.4	360	9	HSTOP015	X93769 H.sapiens m
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38	272.8	78.4	360	9	HSTOP028	X93775 H.sapiens m
39	272.8	78.4	360	9	HSTOP102	X93781 H.sapiens m
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ALIGNMENTS

RESULT 1	AX010614	AX010614	348 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX010614	Sequence 17 from Patent WO9558679.				
DEFINITION	AX010614					
ACCESSION	AX010614					
VERSION	AX010614.1	GI:9997425				
KEYWORDS		synthetic construct.				
SOURCE		artificial sequences.				
ORGANISM		1 (bases 1 to 348)				
REFERENCE		Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.				
AUTHORS		Antibodies to cd23, derivatives thereof, and their therapeutic uses				
TITLE		Patent: WO 9558679-A 17 18-NOV-1999;				
JOURNAL		BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON				

```

NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)
Location/Qualifiers
1..348
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Humanised anti-CD23 antibody light chain variable
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/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:9997426"
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BASE COUNT      81 a      87 c      97 g      83 t
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Best Local Similarity 100.0%; Pred. No. 9.2e-104;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TACCTGCAGAGCCAGGCGGAGTCTCCACAGCTCTCTATCTATTGTGATGCCACCGGGCA 180
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RESULT 2
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LOCUS      348 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9958679.
ACCESSION AX010645
VERSION AX010645.1 GI:9997454
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 348)
AUTHORS Bonneyo,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 48 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)
Location/Qualifiers
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/note="Humanised anti-CD23 antibody light chain variable
region"
BASE COUNT      83 a      97 c      87 g      81 t

NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.2e-104;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
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RESULT 3
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LOCUS      740 bp      DNA      linear      PAT 22-FEB-2001
DEFINITION Sequence 1 from Patent WO0107082.
ACCESSION AX076853
VERSION AX076853.1 GI:13121524
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 740)
AUTHORS Knick,V.C., Stimmel,J.B. and Thurmond,L.M.
TITLE Combination of an anti-ep-cam antibody with a chemotherapeutic
agent
JOURNAL Patent: WO 0107082-A 1 01-FEB-2001;
GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Query Match      83.9%; Score 292; DB 6; Length 740;
Best Local Similarity 89.9%; Pred. No. 3.3e-85;
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QY	301	TTACAGTTCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT	348
Db	381	CGGAGTTCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT	428
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LOCUS	AX076855	740 bp	DNA linear PAT 22-FEB-2001
DEFINITION	Sequence 3 from Patent WO0107082.		
ACCESSION	AX076855		
VERSION	AX076855.1 GI:13121526		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 740)		
AUTHORS	Knick, V.C., Stimmel, J.B. and Thurmond, L.M.		
TITLE	Combination of an anti-ep-cam antibody with a chemotherapeutic agent		
JOURNAL	Patent: WO 0107082-A 3 01-FEB-2001;		
FEATURES	GLAXO GROUP LIMITED (GB)		
	Location/Qualifiers		
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BASE COUNT	/organism="synthetic construct"		
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Best Local Similarity 89.9%; Pred. No. 3.3e-95;			
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;			
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LOCUS DEFINITION	X72467.1	G1:441402				
ACCESSION	C-region; immunoglobulin; J-segment; kappa light chain; V-region.					
KEYWORDS	Homo sapiens					
SOURCE ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1 (bases 1 to 410)					
AUTHORS	Zachau,H.G.					
TITLE	Direct Submission					
JOURNAL	Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG					
REFERENCE	2 (bases 1 to 410)					
AUTHORS	Klein,R., Jaenichen,R. and Zachau,H.G.					
TITLE	Expressed human immunoglobulin kappa genes and their hypermutation					
JOURNAL	Eur. J. Immunol. 23 (12), 3248-3262 (1993)					
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QY	61	ATCTCCTGTCGTCGAGTAAGAGTCCTCTGTATAAGGATGGGAACACATCTTGAATTGG	120			
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QY	121	TACCTCGAGAAGCCAGGGCAGTCCTCACAGCTCTGTGATCTATTTGATGTCCCACCGGGCA	180			
Db	181	TACCTCGAGAAGCCAGGGCAGTCCTCACAGCTCTCTATTTTGGGTTCTAATCGGGCC	240			
QY	181	TCAGGGGTCCTTCACAGTTCAGTGGCAGTCAGGCACAGATTTTACACTGAAATC	240			
Db	241	TCGGGGTCCTTCACAGTTCAGTGGCAGTCAGGCACAGATTTTACACTGAAATC	300			
QY	241	AGCAGAGTGGAGGCTCAGGATGTTGGGTTTTATTACTGTCAACAGCTGGTAGATNCCA	300			

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Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGTTTATTACTGTCATGCAAGCTCTACAAACTCGG 360
QY 301 TTCACGTTGGCCCAAGGACCAAGGTGAGATCAAAAGTACGTTGGCT 348
Db 361 TGGACGTTGGCCCAAGGACCAAGGTGGAATCAACGAAGTGTGGCT 408

RESULT 6
HSA272080
LOCUS
DEFINITION
Homo sapiens partial mRNA for Immunoglobulin light chain variable
region -Anti-F(ab')2 autoantibody (IGVL gene), isolate SN3.
ACCESSION
AJ272080
VERSION
AJ272080.1 GI:7024356
KEYWORDS
anti-F(ab')2; autoantibody; IGVL gene; immunoglobulin; light chain;
variable region.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Elagib,K.E., Borretzen,M., Vatn,I., Natvig,J.B. and Thompson,K.M.
Characterization and V(H) sequences of human monoclonal
anti-F(ab')2 autoantibodies from normals and Sjogren's syndrome
patients
Clin. Immunol. 98 (1), 62-69 (2001)
JOURNAL
MEDLINE
20581359
PUBMED
11141328
REFERENCE
2 (bases 1 to 353)
Elagib,K.E.
Direct Submission
Submitted (21-FEB-2000) Elagib K.E., Laboratory for Rheumatology
Research, Institute of Immunology, Fr. Qvamsgate 1, N-172 Oslo,
NORWAY
FEATURES
Source
1..353
/organism="Homo sapiens"
/isoate="SN3"
/db_xref="taxon:9606"
/germline
1..353
/gene="IGVL"
<1..>353
/function="Anti-F(ab')2 autoantibody"
/codon_start=1
/evidence=experimental
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/protein_id="CAB75876.1"
/db_xref="GI:7024357"
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/translation="DIVMQLSPSLPVTGCEPASISCRSSQSLHNSGNYLDWYLOK
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BASE COUNT 81 a 94 c 93 g 85 t
ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 353;
Best Local Similarity 87.1%; Pred. No. 6.1e-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCTCCTCCACTCTCCCTGCCCTGCACCTCGAGAGCGGCGCTCC 60
Db 1 GATATTGTGATGACTCTCCTCCACTCTCCCTGCCCTGCACCTCGAGAGCGGCGCTCC 60
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Db 61 ATCTCTGTCGCTCGCATGAAGAGTCTCTCTGTATGAAGATGGGAAGACATCTGTAATTCG 120
QY 121 TACCTGCAGAACCCAGGACGTCCTCCACAGCTGCTGATCTATTGTTGATGCCACCGGGCA 180
Db 121 TACCTGCAGAACCCAGGACGTCCTCCACAGCTGCTGATCTATTGTTGATGCCACCGGGCC 180

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QY 181 TCAGGGGTCCCTCAGAGGTTCAAGTGGATCAGGCAGACAGATTTTACACTGAAATC 240
Db 181 TCAGGGGTCCCTCAGAGGTTCAAGTGGATCAGGCAGACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCACACAGCTGGTAGATATCCA 300
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCACACAGCTGGTAGATATCCA 300
QY 301 TTCAAGTTCGGCCCAAGGACCAAGGTGAGATCAAAAGTACGTTGGCT 348
Db 301 CSTACGTTGGCCCAAGGACCAAGGTGGAATCAACGAAGTGTGGCT 348

RESULT 7
HSTOP003
LOCUS
DEFINITION
H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
clone HSTOP003).
ACCESSION
X93771
VERSION
X93771.1 GI:3928404
KEYWORDS
constant region; immunoglobulin; immunoglobulin kappa chain;
immunoglobulin light chain; joining region; variable region.
SOURCE
Homo sapiens.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 360)
Barington,T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
REFERENCE
2 (bases 1 to 360)
Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
Heilmann,C. and Svejgaard,A.
The progeny of a single virgin B cell predominates the human recall
B cell response to the capsular polysaccharide of Haemophilus
Influenzae type b
J. Immunol. 157 (9), 4016-4027 (1996)
JOURNAL
MEDLINE
97047794
PUBMED
8892635
COMMENT
On Nov 26, 1998 this sequence version replaced gi:1296757.
FEATURES
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/tissue_type="peripheral blood"
/rearranged
1..339
/gene="V-kappa-A3/A19 and J-kappa-3"
<1..339
/gene="V-kappa-A3/A19 and J-kappa-3"
/product="immunoglobulin kappa light chain"
/note="variable region and joining region"
340..>360
/region
/region
/region="constant region"
BASE COUNT 81 a 96 c 92 g 91 t
ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 360;
Best Local Similarity 87.1%; Pred. No. 6.1e-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCTCCTCCACTCTCCCTGCCCTGCACCTCGAGAGCGGCGCTCC 60
Db 1 GATATTGTGATGACTCTCCTCCACTCTCCCTGCCCTGCACCTCGAGAGCGGCGCTCC 60
QY 61 ATCTCTGTCGCTCGCATGAAGAGTCTCTCTGTATGAAGATGGGAAGACATCTGTAATTCG 120

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Db 61 ATCTCTGAGGCTAGTCAGAGCCCTCTGTCATAGTATGAATACTATTGGATTGG 120
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Db 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGGTTCTTAATCGGGCC 180
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGCAGTCAGTCAGGACAGATTTTACACTGAAATC 240
Db 181 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGCAGTCAGTCAGGACAGATTTTACACTGAAATC 240
QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTACACTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACCGTGGCT 348
Db 301 TTCACTTCGGCCCTGGGACCAAGTGGATATCAACAGAACTGTGGCT 348

RESULT 8
HSTOP016 360 bp mRNA linear PRI 25-NOV-1998
LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
DEFINITION clone HSTOP016).
ACCESSION X93774
VERSION X93774.1 GI:3928407
KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain;
immunoglobulin light chain; joining region; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Barington,T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
2 (bases 1 to 360)
Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
Heilmann,C. and Svejgaard,A.
The progeny of a single virgin B cell predominates the human recall
B cell response to the capsular polysaccharide of Haemophilus
influenzae type b
J. Immunol. 157 (9), 4016-4027 (1996)
97047794
MEDLINE 8892635
PUBMED
COMMENT On Nov 26, 1998 this sequence version replaced gi:1296760.
FEATURES
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/db_xref="taxon:9606"
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/tissue_type="peripheral blood"
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1..339
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1..339
C_region
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1..339
BASE COUNT 81 a 101 c 90 g 88 t
ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 360;
Best Local Similarity 87.1%; Pred. No. 6,1e-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCCTCC 60
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Db 1 GATATTGTGATGACTCTCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCCTCC 60
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Db 61 ATCTCTCTGCTCGCTGAGTAAGTCTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
Db 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGCAGTCAGTCAGGACAGATTTTACACTGAAATC 240
Db 181 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGCAGTCAGTCAGGACAGATTTTACACTGAAATC 240
QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTACACTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACCGTGGCT 348
Db 301 TTCACTTCGGCCCTGGGACCAAGTGGATATCAACAGAACTGTGGCT 348

RESULT 9
HSTOP019 360 bp mRNA linear PRI 25-NOV-1998
LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
DEFINITION clone HSTOP019).
ACCESSION X93776
VERSION X93776.1 GI:3928409
KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain;
immunoglobulin light chain; joining region; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Barington,T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
2 (bases 1 to 360)
Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
Heilmann,C. and Svejgaard,A.
The progeny of a single virgin B cell predominates the human recall
B cell response to the capsular polysaccharide of Haemophilus
influenzae type b
J. Immunol. 157 (9), 4016-4027 (1996)
97047794
MEDLINE 8892635
PUBMED
COMMENT On Nov 26, 1998 this sequence version replaced gi:1296762.
FEATURES
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/tissue_type="peripheral blood"
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V_region
/clone="TOP019"
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/tissue_type="peripheral blood"
/rearranged
1..339
C_region
/clone="TOP019"
/cell_type="B lymphocyte"
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1..339
BASE COUNT 82 a 95 c 92 g 91 t
ORIGIN
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REFERENCE      1 (bases 1 to 360)
AUTHORS        Barrington,T.
TITLE          Direct Submission
JOURNAL        Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
                7631, Rigshospitalet, National University Hospital, Tagensvej 20,
                DK-2200 Copenhagen N, DENMARK
REFERENCE      2 (bases 1 to 360)
AUTHORS        Barrington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
                Heilmann,C. and Svejgaard,A.
TITLE          The progeny of a single virgin B cell predominates the human recall
                B cell response to the capsular polysaccharide of Haemophilus
                influenzae type b
JOURNAL        J. Immunol. 157 (9), 4016-4027 (1996)
MEDLINE        97047794
PUBMED         8892635
COMMENT        On Nov 26, 1998 this sequence version replaced gi:1296758.
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    /tissue_type="peripheral blood"
    /rearranged
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    /gene="V-kappa-A3/A19 and J-kappa-3"
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    /gene="V-kappa-A3/A19 and J-kappa-3"
    /product="immunoglobulin kappa light chain"
    /note="variable region and joining region"
    340..>360
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gene
V_region
C_region
BASE COUNT    81 a 102 c 89 g 88 t
ORIGIN

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Best Local Similarity 86.88; Pred. No. 2.le-79;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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    |||||
DB  1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGCGCTCC 60

QY  61 ATCTCTCTCGCTCAGTAGAGTCTCTCTGTATAGAGTGGGAGACATCTTGAATTGG 120
    |||||
DB  61 ATCTCTCGAGTCTAGTCAGAGCTCTCTGATAGTAATGGCAACATCTATTTCGATTGG 120

QY  121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCGGGCA 180
    |||||
DB  121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCGGGCC 180

QY  181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
    |||||
DB  181 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

QY  241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
    |||||
DB  241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

QY  301 TTCAGCTTGGGCCAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
    |||||
DB  301 TTCAGCTTGGGCCCTGGGACCAAGTGGATATCAAAAGTACGGTGGCT 348

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Search completed: April 26, 2003, 06:31:05
 Job time : 696.74 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 460.431 Seconds

(without alignments)

12240.775 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtgatcactcagtc.....agatacaacgtacgtggct 348

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estom:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.6	79.8	990	BI838327	BI838327 603083265
2	272.8	78.4	454	10 AW406883	AW406883 UI-HF-BLO
3	272.8	78.4	995	14 BQ712430	BQ712430 AGENCOURT
4	271.2	77.9	522	13 BM511309	BM511309 ij46b08.y
5	269.6	77.5	751	12 BG542438	BG542438 602569513
6	268.2	77.1	363	9 AA464313	AA464313 zx78cl2.r

7	268	77.0	442	9	AA405415	AA405415 zu56d02.y
8	268	77.0	488	10	AW405725	AW405725 UI-HF-BLO
9	268	77.0	634	14	BM783161	BM783161 K-EST0061
10	267	76.7	491	12	BF174573	BF174573 MYE3409a
11	266.4	76.6	456	10	AW404683	AW404683 UI-HF-BLO
12	265	76.1	425	9	AI734035	AI734035 zu56d02.y
13	264.8	76.1	880	12	BG755003	BG755003 602711509
14	264.8	76.1	880	12	BG755888	BG755888 602714763
15	264.8	76.1	926	12	BG342051	BG342051 602463190
16	263.2	75.6	787	12	BG536224	BG536224 602565445
17	261.8	75.2	770	12	BG530186	BG530186 602558684
18	260	74.7	643	14	BM620052	BM620052 K-EST0088
19	259.6	74.6	410	12	BG059215	BG059215 nah51907
20	259	74.4	468	12	BE829853	BE829853 RC6-ET007
21	259	74.4	908	12	BG685179	BG685179 602637065
22	256.8	73.8	462	12	BF176195	BF176195 MYE6594a
23	256	73.6	427	12	BF174767	BF174767 MYE3784.M
24	256	73.6	485	12	BF174421	BF174421 MYE3134a
25	255	73.3	958	14	BQ709417	BQ709417 AGENCOURT
26	254.4	73.1	730	13	BI837183	BI837183 603089959
27	254	73.0	474	12	BF175068	BF175068 MYE4339.M
28	253.6	72.9	952	12	BG758592	BG758592 602712820
29	252	72.4	597	12	BF868788	BF868788 IL3-ET011
30	252	72.4	650	13	BI765629	BI765629 603043768
31	252	72.4	898	14	BQ708918	BQ708918 AGENCOURT
32	252	72.4	960	14	BQ711007	BQ711007 AGENCOURT
33	251.2	72.2	859	12	BG758795	BG758795 602713155
34	250.8	72.1	488	14	H25625	H25625 Y44805.F1
35	248.8	71.5	492	12	BF870113	BF870113 IL3-ET011
36	248	71.3	424	12	BF176198	BF176198 MYE6598a
37	248	71.3	753	12	BG756401	BG756401 602715727
38	247.2	71.0	471	10	AW405772	AW405772 UI-HF-BLO
39	247.2	71.0	614	10	AW405187	AW405187 UI-HF-BLO
40	245.8	70.6	1220	14	BQ708355	BQ708355 AGENCOURT
41	245	70.4	931	12	BG757255	BG757255 602715238
42	241.8	69.5	475	12	BF174510	BF174510 MYE5291a
43	241.2	69.3	824	13	BI824708	BI824708 603033871
44	239.2	68.7	696	13	BI838136	BI838136 603083638
45	239.2	68.7	701	12	BG547597	BG547597 602575437

ALIGNMENTS

RESULT 1	BI838327	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
LOCUS	BI838327	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
DEFINITION	BI838327	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
ACCESSION	BI838327	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
VERSION	BI838327.1	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
KEYWORDS	EST.	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
SOURCE	human.	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
ORGANISM	Homo sapiens	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
REFERENCE	1 (bases 1 to 990)	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
AUTHORS	NIH-MGC	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
JOURNAL	Unpublished (1999)	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11559 row: a column: 18 High quality sequence stop: 740. Location/Qualifiers 1. .990	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001
FEATURES	source	603083265F1	NIH_MGC_120	Homo sapiens	cdna	linear	EST 04-OCT-2001

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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3061493"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="Dh10B (LT1)"
/notice="vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
104 a 122 c 114 g 114 t
BASE COUNT

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Query Match	78.4%	Score 272.8;	DB 10;	Length 454;
Best Local Similarity	86.5%	Pred. No. 1.5e-71;		
Matches 301;	Conservative 0;	Mismatches 47;	Indels 0;	Gaps 0;
Qy 1	GATATTGTGATGACTTCACACTCTCCCTGCCGCTCACCCCTGGAGACCGGCGCTCC	60		
Db 16	GATATTGTGATGACTTCACACTCTCCCTGCCGCTCACCCCTGGAGACCGGCGCTCC	75		
Qy 61	ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG	120		
Db 76	ATCTCCTGCAGGTCTPAGTCAGAGCCTCTCGATAGTAATGGATACAACCTATTTTGGATTGG	135		
Qy 121	TACCTGCAGAGCCAGGCGACTCTCCACAGCTCCTGATCTATTTGATGCCACCGCGCA	180		
Db 136	TACCTGCAGAGCCAGGCGACTCTCCACAGCTCCTGATCTATTTTGGGTTCTATCGGGCC	195		
Qy 181	TCAGGGGTCCTTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240		
Db 196	TCCGGGCTCCCTTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	255		
Qy 241	AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300		
Db 256	ACAAAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAGAGCTCTACAAACTCCT	315		
Qy 301	TTTCACTTTCGGCCAAAGGACCACAGGTGGAGATCAAAAGCTACGGTGGCT	348		
Db 316	CAGACGTTTCGGCCAAAGGACCACAGGTGCAATCAAAAGCAACTGTGGCT	363		

RESULT	3
LOCUS	BQ712430
DEFINITION	BQ712430 linear mRNA EST 16-JUL-2002 AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729 5' , mRNA sequence.
ACCESSION	BQ712430
VERSION	BQ712430.1 GI:21851329
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NIH-MGSC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC). Unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov
TITLE	Tissue Procurement: Dr. Mark Watson
JOURNAL	cDNA Library Preparation: Rubin Laboratory
COMMENT	CNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone Distribution: Agencourt Bioscience Corporation Found through the I.M.A.G.E. Consortium information can be http://image.llnl.gov plate: LICM2464 row: 1 column: 02

[illegible]

```

QY 241 ACACAGTGGAGGCTGAGGATGTTGGGGTTATTACTCTCAACAGCTGTAGAGTATCCA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 ACACAGTGGAGGCTGAGGATGTTGGGGTTATTACTCTCAACAGCTGTAGAGTATCCA 344
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCAGCTTGGCCCAAGGACCAAGTGGAGATCAAAACGCTACGGTGGCT 348
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 345 ATCACCTTGGCCCAAGGACCAAGTGGAGATTAACGAACCTGTGGCT 392
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
BM783161
LOCUS BM783161 634 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0061018 S18N669761 Homo sapiens cDNA clone S18N669761-3-E01
5', mRNA sequence.
ACCESSION BM783161
VERSION BM783161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 634)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 3 row: E column: 01
High quality sequence stop: 634.

FEATURES
SOURCE
1..634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S18N669761-3-E01"
/sex="F"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 153 a 171 c 161 g 149 t
ORIGIN
Query Match 77.0%; Score 268; DB 14; Length 634;
Best Local Similarity 85.6%; Pred. No. 4.9e-70;
Matches 298; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 GATATTGTGAGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCGCTCC 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 GACATTGTGAGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCGCTCC 158
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATCTCCTGCTGCTGAGTAAAGAGTCTCCTGTATAGGATGGGAACATACACTTGAATTGG 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 159 ATCTCCTGCAAGTCTAGTCAGAGCCTCTACATAGTAATGGAATACAACATAATTGAATTGG 218
QY 121 TACCTGCAGAACCCAGGCGAGCTCCACAGCTCCTCATCTATTTGATGTCCACCCGGGCA 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 219 TTCTCTGCAGAACCCAGGCGAGCTCCACAGATCCTCATCTATTTGCTTCTAATCGGGCC 278
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 279 TCCGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 338
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTTCAACAGCTGGTAGAGTATCCA 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTTCAACAGCTGGTAGAGTATCCA 398
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCAGCTTGGCCCAAGGACCAAGTGGAGATCAAAACGCTACGGTGGCT 348
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 399 CGGACGTTTCGGCCCAAGGACCAAGTGGAGTCAAACTAAGTCTGGCT 446
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
BM783161
LOCUS BM783161 491 bp mRNA linear EST 23-MAR-2001
DEFINITION MYE3409a Myeloma (MYE) cDNA library Homo sapiens cDNA, mRNA
sequence.
ACCESSION BM783161
VERSION BM783161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 491)
AUTHORS Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Cukerman,E.,
Francisco-Pabalan,O., Liew,C.C. and Stewart,A.K.
TITLE The transcriptional phenotype of myeloma cells
JOURNAL Unpublished (2000)
COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
Email: k.stewart@utoronto.ca
PCR Primers
FORWARD: 5'-GCCAAGCTCAAAATTAACCTCCTCACTAAAGG-3'
BACKWARD: 5'-CCAGTGAATCTTAATCACTCACTACTATAGGCG-3'
Seq primer: 5'-GAAATTAACCTCCTCACTAAAGG-3'.

FEATURES
source
1..491
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Myeloma (MYE) cDNA library"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="multiple myeloma"
/notes="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
XhoI; Myeloma cells from multiple myeloma patients' bone
marrow were purified by magnetic cell sorting. mRNA were
purified and an oligo d(T)18 primer containing XhoI
restriction site was used to prime first strand synthesis
using M-MLV reverse transcriptase. To protect the cDNAs
from XhoI digestion in subsequent cloning step, the
nucleotide analogue 5-methyl-dCTP was added to the
nucleotide mixture and [a-32p]dATP was added to monitor
the quantity and quality of first strand synthesis. After
second-strand synthesis and blunting of cDNA termini,
EcoRI adapters were ligated, followed by kinase treatment
and digestion with XhoI. The cDNAs were then
size-fractionated using Sephacryl S-500 column and then
ligated into EcoRI and XhoI digested Lambda Zap Express
vector. The ligation product was packaged using Gigapack
II packaging extract. The library had primary titre of

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approx. 1x10⁶. Clones from the primary library were randomly selected for single pass sequencing."

BASE COUNT 102 a 136 c 128 g 124 t 1 others

ORIGIN

Query Match 76.7%; Score 267; DB 12; Length 491;
Best Local Similarity 85.3%; Pred. No. 8.6e-70;
Matches 297; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTGCGCTCCACCTGCGCTCCACCTGCGCTCC 60
|||||
DB 81 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTGCGCTCCACCTGCGCTCCACCTGCGCTCC 140
|||||
QY 61 ATCTCTGCTGCGCTGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACCTTTGAATGG 120
|||||
DB 141 ATCTCTGCTGCGCTGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACCTTTGAATGG 200
|||||
QY 121 TACCTGCAGAGCCAGGCGACTCTCCACAGCTCTCTGATCTATTTGATGTCACCCCGGCA 180
|||||
DB 201 TACCTGCAGAGCCAGGCGACTCTCCACAGCTCTCTGATCTATTTGATGTCACCCCGGCA 260
|||||
QY 181 TCAGGGTCCCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||||
DB 261 TCCGGGNCCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 320
|||||
QY 241 ACAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
|||||
DB 321 ACAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 380
|||||
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGCTGGTGGCT 348
|||||
DB 381 CAGACTTTTGGCCAGGGACCAAGTGGAGATCAAAAGTACGCTGGTGGCT 428
|||||

RESULT 11
AW404683
LOCUS
DEFINITION
IMAGE:3058464 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M3 Forward.
Location/Qualifiers
1. .456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058464"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA

FEATURES
source

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 99 a 121 c 117 g 119 t

ORIGIN

Query Match 76.6%; Score 266.4; DB 10; Length 456;
Best Local Similarity 85.3%; Pred. No. 1.3e-69;
Matches 297; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTGCGCTCCACCTGCGCTCCACCTGCGCTCC 60
|||||
DB 21 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTGCGCTCCACCTGCGCTCCACCTGCGCTCC 80
|||||
QY 61 ATCTCTGCTGCGCTGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACCTTTGAATGG 120
|||||
DB 81 ATCTCTGCTGCGCTGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATACCTTTGAATGG 140
|||||
QY 121 TACCTGCAGAGCCAGGCGACTCTCCACAGCTCTCTGATCTATTTGATGTCACCCCGGCA 180
|||||
DB 141 TACCTGCAGAGCCAGGCGACTCTCCACAGCTCTCTGATCTATTTGATGTCACCCCGGCA 200
|||||
QY 181 TCAGGGTCCCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||||
DB 201 TCCGGGTCCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 260
|||||
QY 241 ACAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
|||||
DB 261 ACAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 320
|||||
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGCTGGTGGCT 348
|||||
DB 321 ATCACTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGCTGGTGGCT 368
|||||

RESULT 12
AI734035
LOCUS
DEFINITION
IMAGE:741987 5', similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1997)
Other ESTs: zu56d02.s1
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI human EST Project
This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco.
Insert Length: 1053
Std Error: 0.00
Location/Qualifiers
1. .425
/organism="Homo sapiens"
/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone="IMAGE:741987"
/clone_lib="Soares ovary tumor N6HOT"
/sex="Female"
/tissue_type="ovarian tumor"

FEATURES
source

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/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTGAGTGGGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      88 a 114 c 111 g 112 t
ORIGIN

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Query Match      76.1%; Score 265; DB 9; Length 425;
Best Local Similarity 85.5%; Pred. No. 3.2e-69;
Matches 295; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCGCGCTCC 60
DB 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCATCCCTGGAGAGCGCGCTCC 140

QY 61 ATCTCCTGTGCGTCAGTAGAGTCTCCCTGTATAGGATGGGAAGACATATTGAATTGG 120
DB 141 ATCTCCTGTGCGTCAGTAGAGTCTCCCTGTATAGGATGGGAAGACATATTGAATTGG 200

QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
DB 201 TATCTGAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGGTCTTAATCGGGCC 260

QY 181 TCAGGGTCTCCAGGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
DB 261 TCCGGGTCTCCAGGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 320

QY 241 AGCAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 321 AGCAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 380

QY 301 TTCAGTTCCGACGGGACAGGTGGAGATCAACAGTACAGCTGACGGTG 345
DB 381 CACACTTTGGCCAGGGACAGGTGGAGATCAACAGTACAGCTGACGGTG 425

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RESULT 13
LOCUS      BG755003      880 bp      mRNA      linear      EST 15-MAY-2001
DEFINITION 602711509F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851723 5',
            mRNA sequence.
ACCESSION  BG755003
VERSION    BG755003.1 GI:14065656
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE  1 (bases 1 to 880)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgraphs@email.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI695 row: a column: 04
            High quality sequence stop: 845.
            Location/Qualifiers

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FEATURES
source     1..880
            /organism="Homo sapiens"
            /db_xref="taxon:9606"

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/clone="IMAGE:4851723"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
BASE COUNT      204 a 266 c 216 g 194 t
ORIGIN

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```

Query Match      76.1%; Score 264.8; DB 12; Length 880;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCGCGCTCC 60
DB 71 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCGCGCTCC 130

QY 61 ATCTCCTGTGCGTCAGTAGAGTCTCTCTGTATAAGGATGGGAAGACATATTGAATTGG 120
DB 131 ATCTCCTGTGCGTCAGTAGAGTCTCTCTGTATAAGGATGGGAAGACATATTGAATTGG 190

QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
DB 191 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGGTCTTAATCGGGCC 250

QY 181 TCAGGGTCTCCAGGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
DB 251 TCCGGGTCTCCAGGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 310

QY 241 AGCAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 311 AACAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 370

QY 301 TTCAGTTCCGACGGGACAGGTGGAGATCAACAGTACAGCTGACGGTGCT 348
DB 371 TTCAGTTCCGACGGGACAGGTGGAGATCAACAGTACAGCTGACGGTGCT 418

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RESULT 14
LOCUS      BG757588      880 bp      mRNA      linear      EST 15-MAY-2001
DEFINITION 602714763F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:485095 5',
            mRNA sequence.
ACCESSION  BG757588
VERSION    BG757588.1 GI:14068241
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE  1 (bases 1 to 880)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgraphs@email.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI703 row: m column: 16
            High quality sequence stop: 718.
            Location/Qualifiers

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FEATURES

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source
1. .880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:485095"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/site="EcoRI; B-cells; Vector: pOTB7; Site:1: XhoI;
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 201 a 225 c 223 g 200 t 1 others
ORIGIN
Query Match 76.1%; Score 264.8; DB 12; Length 880;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCGCTGAGAGCGGCTCC 60
DB 71 GAAATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCGCTGAGAGCGGCTCC 130
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGTATTAAGATGGGAGACATCTTGAATTGG 120
DB 131 ATCTCTCTGCTCGAGTCTCCTGATAGCATGATGATGATGATGATGATGATGATG 190
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGATGATGATGATG 180
DB 191 TACCTGCAGAGCCAGGCGAGTCTCCACAACTCTGATCTATTGGTCTTAATCGGGC 250
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGATGATGATGATGATGATGATGATGATG 240
DB 251 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGATGATGATGATGATGATGATGATGATG 310
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGTAGATATCCA 300
DB 311 AACAGATGGAGGCTGACGATGTTGGGGTTTATTACTGTCAACAGCTGTACAACTCC 370
QY 301 TTCAGTTCGCCAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 348
DB 371 TTCAGTTCGCCAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 418

RESULT 15
BG342051 926 bp mRNA linear EST 27-FEB-2001
LOCUS 602463190F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575718 5',
DEFINITION mRNA sequence.
ACCESSION BG342051
VERSION BG342051.1 GI:13148477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```

```

Plate: LLCMI287 row: d column: 23
High quality sequence stop: 558.
FEATURES
Location/Qualifiers
source 1..926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4575718"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/site="EcoRI; B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 221 a 242 c 245 g 218 t
ORIGIN
Query Match 76.1%; Score 264.8; DB 12; Length 926;
Best Local Similarity 87.1%; Pred. No. 5.6e-69;
Matches 303; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCGCTGAGAGCGGCTCC 60
DB 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCGCTGAGAGCGGCTCC 140
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGTATAAGATGGGAGACATCTTGAATTGG 120
DB 141 ATCTCTCTGCTCGAGTCTCCTGATAGCATGATGATGATGATGATGATGATGATG 197
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGATGATGATGATG 180
DB 198 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGATGATGATGATG 257
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGATGATGATGATGATGATGATGATGATG 240
DB 258 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGATGATGATGATGATGATGATGATGATG 317
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGTAGATATCCA 300
DB 318 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGTAGATATCCA 377
QY 301 TTCAGTTCGCCAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 348
DB 378 TGGAGCTTCGCCAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 425

Search completed: April 26, 2003, 07:26:47
Job time : 464.431 secs

```


GenCore version 5.1.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 70.0118 seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtatgactcagtc.....agatcaaacgtacgttggtc 348

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	348	100.0	348	21	Humanised anti-CD22
2	292	83.9	740	22	Humanised 323/A3 (
3	292	83.9	740	22	Anti-Ep-CAM antibo
4	276	79.3	772	20	Human bladder tumo
5	274	78.7	720	21	Human PTHrp monocl
6	273	78.4	720	21	Human PTHrp monocl
7	272.8	78.4	720	21	Human PTHrp monocl
8	272.4	78.3	720	21	Human PTHrp monocl
9	271.8	78.1	720	21	Human PTHrp monocl

10	270.8	77.8	720	21	AAA13926	Human PTHrp monocl
11	269.6	77.5	720	21	AAA13921	Human PTHrp monocl
12	268.2	77.1	720	21	AAA13923	Human PTHrp monocl
13	267.8	77.0	720	21	AAA13929	Human PTHrp monocl
14	266.6	76.6	720	21	AAA13922	Human PTHrp monocl
15	263.2	75.6	963	22	AAF44895	Human breast cance
16	263	75.6	1143	22	AAD20732	Human blyPHI-IL-2
17	262.8	75.5	339	22	AAD20730	Human PFI Fab anti
18	262.8	75.5	663	22	AAD20744	Human recombinant
19	261.2	75.1	339	15	AAQ70940	Anti-CMV monoclon
20	258.8	74.4	342	21	AAZ27664	DNA encoding anti-
21	258.4	74.3	417	22	AAH41159	Human coding seque
22	257.2	73.9	437	21	AAZ34746	Mouse anti-CD23 MA
23	257.2	73.9	744	22	AAH47762	Anti-hEDRF antibod
24	253.4	72.8	651	20	AAZ24421	Human bladder tumo
25	252.8	72.6	336	19	AAV10325	Human Mab ABL7.1.4
26	252	72.4	336	22	AAH68644	Human anti-Rh(D) c
27	251.6	72.3	336	21	AAQ6160	Nucleotide sequenc
28	250.4	72.0	444	20	AAZ20410	Igm antibody CEM 1
29	249.4	71.7	339	17	AAI10942	Vlkappa coding seq
30	245.6	70.6	381	24	ABK48973	DNA encoding light
31	245.6	70.6	720	19	AAV61359	Anti-human Fas hum
32	245.6	70.6	720	21	AAV78267	Anti-human Fas imm
33	244	70.1	420	19	AAV03802	DNA encoding the l
34	244	70.1	464	14	AAQ33097	C242:11 Mab kappa
35	244	70.1	464	14	AAQ36950	C242 kappa chain v
36	244	70.1	720	19	AAV61360	Anti-human Fas hum
37	244	70.1	720	19	AAV61361	Anti-human Fas hum
38	244	70.1	720	21	AAV78268	Anti-human Fas imm
39	244	70.1	720	21	AAV78269	Anti-human Fas imm
40	243.6	70.0	340	19	AAV09791	DNA encoding the l
41	242.4	69.7	720	19	AAV61362	Anti-human Fas hum
42	242.4	69.7	720	21	AAV78270	Anti-human Fas imm
43	242	69.5	793	24	ABK43188	DNA encoding const
44	242	69.5	1111	24	ABK43191	DNA encoding fiber
45	242	69.5	1402	24	ABK43192	DNA encoding fiber

ALIGNMENTS

RESULT 1
AAZ34747
ID AAZ34747 standard; cDNA; 348 BP.
XX AC
XX AAZ34747;
XX
DT 15-FEB-2000 (first entry)
XX
DE Humanised anti-CD23 Mab C11 light chain variable region cDNA.
XX
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO9958679-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB01434.
XX
XX 09-MAY-1998; 98GB-0009839.
XX

PA (GLAX) GLAXO GROUP LTD.
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI: 2000-053101/04.
 XX P-PSDB; AAY32262.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX
 XX Claim 17; Fig 3; 81pp; English.
 XX
 CC This DNA sequence encodes the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of
 CC a human framework (H5ICKVII) and the light chain complementarity
 CC determining regions (see AAY32254-56) of murine antibody C11. The
 CC DNA was constructed by splice overlap PCR. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies, which
 CC comprise sufficient of the amino acid sequences of the C11 light
 CC and heavy chain complementarity determining regions to render them
 CC capable of binding to the CD23 type II molecule expressed on
 CC hematopoietic cells. The antibodies are used to block soluble
 CC CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis,
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 XX Sequence 348 BP; 81 A; 87 C; 97 G; 83 T; 0 other;
 XX
 XX Query Match 100.0%; Score 348; DB 21; Length 348;
 XX Best Local Similarity 100.0%; Pred. No. 6.1e-98;
 XX Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 GATATTGTGATGACCTCAGCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 60
 Db 1 GATATTGTGATGACTAGCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 60
 QY 61 ATCTCCTGTGCTCGAGTAGAGTCTCCTGTATAAGATGGGAGACATCTTGAATTGG 120
 Db 61 ATCTCCTGTGCTCGAGTAGAGTCTCCTGTATAAGATGGGAGACATCTTGAATTGG 120
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180
 Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180
 QY 181 TCAGGGTCTCCTGACAGTTTCAGTGGCAGTGGATGATGATGATTTTACACTGAAATC 240
 Db 181 TCAGGGTCTCCTGACAGTTTCAGTGGCAGTGGATGATGATGATTTTACACTGAAATC 240
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCA 300
 Db 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCA 300
 QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348
 Db 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348
 XX
 XX RESULT 2
 XX AAF63373
 XX ID AAF63373 standard; cDNA; 740 BP.
 XX AC AAF63373;
 XX DT 10-MAY-2001 (first entry)
 XX

DE Humanised 323/A3 (IgG1) antibody light chain cDNA sequence.
 XX
 KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
 KW Chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
 KW Light chain; ss.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO200107082-A1.
 XX
 PD 01-FEB-2001.
 XX
 XX 23-JUL-1999; 99WO-EP05271.
 XX
 PR 23-JUL-1999; 99WO-EP05271.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 XX Knick VC, Stimmel JB, Thurmond LM;
 PI
 XX WPI: 2001-182729/18.
 XX P-PSDB; AAB72227.
 XX
 PT Combination for treating cancer (e.g. breast, gastric or prostate
 PT cancers), or in the manufacture of a medicament for anti-cancer
 PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
 PT with a chemotherapeutic agent -
 XX
 XX Example 6; Fig 15; 103pp; English.
 XX
 CC This invention relates to a combination of an anti-Ep-CAM (cyclic
 CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
 CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
 CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
 CC replication. The antibody exhibits cytostatic activity and is useful in
 CC the manufacture of a medicament for use in anti-cancer therapy,
 CC characterised in that a chemotherapeutic agent, which is capable of
 CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
 CC co-administered to a patient with an anti-Ep-CAM antibody. The
 CC combination is useful for treating cancer, particularly colorectal
 CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents cDNA encoding the light
 CC chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can
 CC be used in the combination of the invention.
 XX
 XX Sequence 740 BP; 187 A; 201 C; 187 G; 165 T; 0 other;
 XX
 XX Query Match 83.9%; Score 292; DB 22; Length 740;
 XX Best Local Similarity 89.9%; Pred. No. 1.8e-80;
 XX Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 XX
 QY 1 GATATTGTGATGACCTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 60
 Db 81 GATATTGTGATGACTAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 140
 QY 61 ATCTCCTGTGCTCGAGTAGAGTCTCCTGTATAAGATGGGAGACATCTTGAATTGG 120
 Db 141 ATCTCCTGTGCTCGAGTAGAGTCTCCTGTATAAGATGGGAGACATCTTGAATTGG 200
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180
 Db 201 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGCCACCGGGCA 260
 QY 181 TCAGGGTCTCCTGACAGTTTCAGTGGCAGTGGATGATGATGATTTTACACTGAAATC 240
 Db 261 TCAGGGTCTCCTGACAGTTTCAGTGGCAGTGGATGATGATGATTTTACACTGAAATC 320
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 Db 321 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCTCAAACTAGAGATTCCT 380
 QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348

```
|||||
Db 381 CGGACGTTCCGCGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 428
|||||

RESULT 3
AAF63377/c
ID AAF63377 standard; DNA; 740 BP.
XX
AC AAF63377;
XX
DT 10-MAY-2001 (first entry)
XX
DE Anti-Ep-CAM antibody related DNA sequence SEQ ID 3.
XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer; ds.
XX
OS Unidentified.
XX
PN WO200107082-A1.
XX
PD 01-FEB-2001.
XX
PF 23-JUL-1999; 99WO-EP05271.
XX
PR 23-JUL-1999; 99WO-EP05271.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Knick VC, Stimmel JB, Thurmond LM;
XX
DR WPI; 2001-182729/18.
XX
PT Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
PS Disclosure; Page 66; 103pp; English.
XX
CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy.
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents DNA related to the
CC anti-Ep-CAM antibody used in the combination of the invention.
XX
SQ Sequence 740 BP; 165 A; 187 C; 201 G; 187 T; 0 other;

Query Match 83.9%; Score 292; DB 22; Length 740;
Best Local Similarity 89.9%; Pred. No. 1.8e-80;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 60
|||||
Db 660 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 601
|||||
QY 61 ATCTCTGTGCTCGTCAAGTAAAGTCTCTGTATAGGATGGGAACATACCTTGATGG 120
|||||
Db 600 ATCTCTGTAGTGTCTAGTAAAGATCTCTGTGCATGTAATGGCATCACTATTGTGATGG 541
|||||
QY 121 TACCTCGAAGCGAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGATCCACCGCGCA 180
|||||
Db 540 TACCTCGAAGCGAGGCGAGTCTCCACAGCTCCTGATCTATCAGATGTCCAACTTGC 481
|||||
QY 181 TCAGGGGTCCCTGACAGGTTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||||

Db 480 TCAGGGGTCCCTGACAGGTTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 421
|||||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCACAGAGTGGTAGAGTATCCA 300
|||||
Db 420 AGCAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCCTCAAAATCTAGAGATTCCT 361
|||||
QY 301 TTCACGTTGCGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
|||||
Db 360 CGGACGTTGCGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 313
|||||

RESULT 4
AAZ24418
ID AAZ24418 standard; cDNA; 772 BP.
XX
AC AAZ24418;
XX
DT 14-FEB-2000 (first entry)
XX
DE Human bladder tumour cDNA library derived EST 30.
XX
KW Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
KW treatment; gene therapy; EST; ss.
XX
OS Homo sapiens.
XX
PN DE19818619-A1.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1998; 98DE-1018619.
XX
PR 21-APR-1998; 98DE-1018619.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-612028/53.
XX
PT New nucleic acid sequences expressed in bladder tumor tissue, and
PT derived polypeptides, for treatment of bladder tumor and identification
PT of therapeutic agents -
XX
PS Claim 3; Page 84; 132pp; German.
XX
CC This invention describes novel polypeptide fragments (I) and the
CC polynucleotides (II) that encode them that are highly expressed in a
CC human bladder tumour and which have cytostatic activity. (II) are used
CC for recombinant expression of (I) and to isolate complete genes. (I) are
CC used to identify agents suitable for treatment of bladder cancer, to
CC directly treat this form of cancer (including expression from gene
CC therapy vectors) or are used in a preparation for cancer treatment. (I)
CC is also used for the generation of specific antibodies. (II) are
CC identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of the gene to be revealed, and
CC allows a significantly longer fragment of the gene to be revealed, and
CC therefore reduces the number of failures associated with the fact that
CC ESTs from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AAZ43260-243309 represent expressed sequence tag (EST)
CC fragments isolated from a human bladder tumour cDNA library which encode
CC the proteins represented in AAY66143-Y66198.
XX
SQ Sequence 772 BP; 181 A; 210 C; 206 G; 175 T; 0 other;

Query Match 79.3%; Score 276; DB 20; Length 772;
Best Local Similarity 87.1%; Pred. No. 1.7e-75;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 60
|||||
```

```
Db 87 GATATTGTGACTCAGTCTCCACTCTCCCTGCCCTCACCCTGGAGAGCGGCTCC 146
QY 61 ATCTCTGTCTGCTGAGTCTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 ATCTCTGCTGAGTCTAGTCAGAGCTCTCTGCATAGTAATGGATACAACTATTTGGATTGG 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCCACCGGGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGGGTTCTTAATCGGGCC 266
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 TCCGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTACAACTCCT 386
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCAGGTTCCGCCAAGGCAAGGTGGAGATCAAACTGACGTGGCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 387 CTCACCTTCGGCGGAGGCAAGGTGGAGATCAAACTGACGTGGCT 434

RESULT 5
AAAL3927
ID AAAL3927 standard; DNA; 720 BP.
XX
AC AAAL3927;
XX
XX 02-AUG-2000 (first entry)
DT
DE Human PTHrP monoclonal antibody clone 3G4-3 DNA SEQ ID NO:17.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
OS Homo sapiens.
XX
XX JP2000080100-A.
PN
XX 21-MAR-2000.
PD
PF 12-OCT-1998; 98JP-0304793.
XX
PR 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX P-PSDB; AAY82617.
XX
PT A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Example 10; Page 50; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone nucleotide sequence from the
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CC present invention.
XX
SQ Sequence 720 BP; 174 A; 191 C; 188 G; 163 T; 4 other;
Query Match 78.7%; Score 274; DB 21; Length 720;
Best Local Similarity 86.5%; Pred. No. 7e-75;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTGGAGAGCGGCTCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GATATTGTGATGACTCAGTNTCCACTCTCCCTGCCCTGAGAGCGGCTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATCTCTGTCTGCTGAGTCTCTCTGTATAGGATGGGAGACATATCTTGAATTGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATTTCTCTGAGTCTAGTCAGAGCTCTCTGATAGTAATGGAAACAACATTTTGGATTGG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCCACCGGGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGGGTTCTTAATCGGGCC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TCCGGGTTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTACAACTCCT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCAGGTTCCGCCAAGGCAAGGTGGAGATCAAACTGACGTGGCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 TTCACCTTCGGCGGAGGCAAGGTGGAGATCAAACTGACGTGGCT 408

RESULT 6
AAAL3924
ID AAAL3924 standard; DNA; 720 BP.
XX
AC AAAL3924;
XX
XX 02-AUG-2000 (first entry)
DT
DE Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
OS Homo sapiens.
XX
XX JP2000080100-A.
PN
XX 21-MAR-2000.
PD
PF 12-OCT-1998; 98JP-0304793.
XX
PR 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX P-PSDB; AAY82614.
XX
PT A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Example 10; Page 41-42; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
```


CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 174 A; 190 C; 188 G; 163 T; 5 other;

Query Match 78.4%; Score 273; DB 21; Length 720;
 Best Local Similarity 86.2%; Pred. No. 1.4e-74;
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACTCTCTGGAGAGCGCGCTCC 60
 Db 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCGCCGTCACTCTCTGGAGAGCGCGCTCC 120

QY 61 ATCTCCTGCTCGTCCAGTAAGAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 120
 Db 121 ATCTCCTGCTCGTCCAGTAAGAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 180

QY 121 TACCTGCAGAACGCGGAGTCTCCACAGCTCTCTGTATAGGATGGAGACATACCTGAATTGG 180
 Db 181 TACCTGCAGAACGCGGAGTCTCCACAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 240

QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 240
 Db 241 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 300

QY 241 AGCAGAGTGGAGCTGAGATCTGGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 300
 Db 301 AGCAGAGTGGAGCTGAGATCTGGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 360

QY 301 TTCACGTTCCGCGCAAGGACCAAGTGGAGATCAACAGCTACCGTGGCT 348
 Db 361 TTCACGTTCCGCGCGTGGACCAAGTGGAGATCAACAGCTACCGTGGCT 408

RESULT 7
 ID AAA13925 standard; DNA; 720 BP.
 XX
 AC AAA13925;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 1C1-3 DNA SEQ ID NO:13.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NIBS) JAPAN TOBACCO INC.
 XX
 DE WPI; 2000-286723/25.

DR P-PSDB; AAY82615.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 XX Example 10; Page 44-45; 88pp; Japanese.
 XX
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 172 A; 197 C; 190 G; 160 T; 1 other;

Query Match 78.4%; Score 272.8; DB 21; Length 720;
 Best Local Similarity 86.5%; Pred. No. 1.6e-74;
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACTCTCCAGAGCGCGCTCC 60
 Db 61 GATATTGTGATGACTCAGTCTCCCTGCGCCGTCACTCTCCAGAGCGCGCTCC 120

QY 61 ATCTCCTGCTCGTCCAGTAAGAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 120
 Db 121 ATCTCCTGCTCGTCCAGTAAGAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 180

QY 121 TACCTGCAGAACGCGGAGTCTCCACAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 180
 Db 181 TACCTGCAGAACGCGGAGTCTCCACAGTCTCTGTATAGGATGGAGACATACCTGAATTGG 240

QY 181 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 240
 Db 241 TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATTC 300

QY 241 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 300
 Db 301 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 360

QY 301 TTCACGTTCCGCGCAAGGACCAAGTGGAGATCAACAGCTACCGTGGCT 348
 Db 361 TTCACGTTCCGCGCGTGGACCAAGTGGAGATCAACAGCTACCGTGGCT 408

RESULT 8
 ID AAA13928 standard; DNA; 720 BP.
 XX
 AC AAA13928;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 4B4-6-21 DNA SEQ ID NO:19.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP2000080100-A.
 XX

PD 21-MAR-2000.
 XX 12-OCT-1998; 98JP-0304793.
 PF 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX (NIBS) JAPAN TOBACCO INC.
 PA WPI; 2000-286723/25.
 XX P-PSDB; AAY82618.
 DR A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX Example 10; Page 53-54; 88pp; Japanese.
 XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.
 XX Sequence 720 BP; 174 A; 191 C; 186 G; 162 T; 7 other;
 SQ
 Query Match 78.3%; Score 272.4; DB 21; Length 720;
 Best Local Similarity 86.2%; Pred. No. 2.2e-74;
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 60
 Db 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 120
 QY 61 ATCTCTGTCGCTGAGTAAAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
 Db 121 ATCTCTGTCAGGCTAGTACAGGCTCCTGAATAGTAAAGTAACTATTTCTGATTGG 180
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGCA 180
 Db 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCCTGATCTATTGTTGGTTCTAATCGGGC 240
 QY 181 TCAGGGTCCCTGACAGGTTTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 240
 Db 241 TCCGGGTCCCTGACAGGTTTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTCTCAACAGCTGGTAGATATCCA 300
 Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGATGCAAGCTCTACAACATCCA 360
 QY 301 TTCAGGTTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT 348
 Db 361 TTCAGTTTCGGCCCTGGGACCAAGTGGATATCAACGAACCTGTGGCT 408
 RESULT 9
 AAAL3920
 ID AAAL3920 standard; DNA: 720 BP.
 XX AC
 XX AAAL3920;
 XX 02-AUG-2000 (first entry)
 DT
 XX Human PTHrP monoclonal antibody clone 15H7-8-3 DNA SEQ ID NO:3.
 XX

KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antinflammatory; ds.
 XX Homo sapiens.
 OS JP2000080100-A.
 XX 21-MAR-2000.
 PD 12-OCT-1998; 98JP-0304793.
 PF 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX (NIBS) JAPAN TOBACCO INC.
 PA WPI; 2000-286723/25.
 XX P-PSDB; AAY82610.
 DR A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX Example 10; Page 31-32; 88pp; Japanese.
 XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.
 XX Sequence 720 BP; 174 A; 191 C; 188 G; 164 T; 3 other;
 SQ
 Query Match 78.1%; Score 271.8; DB 21; Length 720;
 Best Local Similarity 86.2%; Pred. No. 3.3e-74;
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 60
 Db 61 GATATTGTGATGACTCAGTNTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 120
 QY 61 ATCTCTGTCGCTGAGTAAAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
 Db 121 ATCTCTGTCAGGTTTAGTCAGAGCTCCTGATAGTAAAGTAACTATTTGATTGG 180
 QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGCA 180
 Db 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCCTGATCTATTGTTGGTTCTAATCGGGC 240
 QY 181 TCAGGGTCCCTGACAGGTTTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 240
 Db 241 TCCGGGTCCCTGACAGGTTTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTCTCAACAGCTGGTAGATATCCA 300
 Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGATGCAAGCTCTACAACATCCA 360
 QY 301 TTCAGGTTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT 348
 Db 361 TTCAGTTTCGGCCCTGGGACCAAGTGGATATCAACGAACCTGTGGCT 408

RESULT 10
 AAA13926
 ID AAA13926 standard; DNA; 720 BP.
 AC
 XX AAA13926;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 264-12-20 DNA SEQ ID NO:15.
 XX
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 XX
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NITSB) JAPAN TOBACCO INC.
 XX
 XX WPI; 2000-286723/25.
 XX
 DR P-PSDB; AAY82616.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein,
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Example 10; Page 48-49; 88pp; Japanese.
 XX
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.
 XX
 SQ Sequence 720 BP; 172 A; 193 C; 187 G; 163 T; 5 other;
 Query Match 77.8%; Score 270.8; DB 21; Length 720;
 Best Local Similarity 85.9%; Pred. No. 6.8e-74;
 Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACAGTCTCCCTCCCGTCCACCCCTGGAGAGCGGCCCTCC 60
 DB 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTCCCGTCCACCCCTGGAGAGCGGCCCTCC 120
 QY 61 ATCTCCTCTGCTCGAGTAGACTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
 DB 121 ATCTCCTCGAGTCTAGTCAGAGCTCTTTCATAGTATGGATACACTATTGTGATTGG 180
 QY 121 TACCTGCAGAGACGAGGCGAGTCTCCACAGTCTCTGATCTATTGTATGTCACCGCGGCA 180
 DB 181 TTCTCTGCAGAGACGAGGCGAGTCTCCACAGTCTCTGATCTATTGTGGTTTCTAATCGGCC 240
 QY 181 TCAGGGGTCCCTGCAGAGTTTCAGTGGCGAGTGGATCAGGCACAGATTTTACCTGAAATC 240
 DB 241 TCGGGGTCCCTGCAGAGTTTCAGTGGCGAGTGGATCAGGCACAGATTTTACCTGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTCAGTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTTACGGTGGCT 348
 DB 361 TTCACTTTCGGCCCTGGGACCAAGTGGATATCAACAGCAACTGTGGCT 408

RESULT 11
 AAA13921
 ID AAA13921 standard; DNA; 720 BP.
 XX

AC AAA13921;
 XX
 DT 02-AUG-2000 (first entry)
 XX

DE Human PTHrP monoclonal antibody clone 16E12-6 DNA SEQ ID NO:5.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.

XX Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX 17-JUN-1998; 98JP-0188196.

XX 26-JUN-1998; 98JP-0196729.

XX (NITSB) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX P-PSDB; AAY82611.

XX A human monoclonal antibody to parathyroid hormone related protein,
 XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 XX including metastasis, and pain

XX Example 10; Page 33-34; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 174 A; 200 C; 187 G; 159 T; 0 other;

Query Match 77.5%; Score 269.6; DB 21; Length 720;

Best Local Similarity 85.9%; Pred. No. 1.6e-73;

Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCCACCCCTGGAGAGCGGCCCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCCACCCCTGGAGAGCGGCCCTCC 120

QY 61 ATCTCCTCTGCTCGCTCCAGTATAGAGTCTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120

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11111111 11111111 11111111 11111111 11111111 11111111 11111111 11111111
121 ATCTCTGCTGAGTCCAGTCAGAGCTCTCTGCATAGAAATGGAACAACTATTGGATTGG 180
121 TACCTGCAGAGCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
181 TTCTTGCAGAGCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 240
181 TCAGGGTCTCTGACAGTCTCAGTGGCAGTGGATGATCAGGACGACAGATTTTACACTGAAATC 240
241 TCCGGGTCCTTCCAGCTTCTCAGTGGCAGTGGATGATCAGGACGACAGATTTTACACTGAAATC 300
241 AGCAGCTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
301 AGCAGCTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360
301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGCTACGGTGGCT 348
361 TTCACTTTCGGCCCTGGACCAAGTGGATATCAACGAACTGTGGCT 408

RESULT 12
AAAL3923
ID AAAL3923 standard; DNA; 720 BP.
AC AAAL3923;
XX
XX
DT 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 184-10-13 DNA SEQ ID NO:9.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
XX Homo sapiens.
XX
XX JF2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX
XX P-PSDB; AAY82613.
XX
XX A human monoclonal antibody to parathyroid hormone related protein,
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Example 10; Page 38-39; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone nucleotide sequence from the
XX present invention.
XX
XX Sequence 720 BP; 174 A; 193 C; 187 G; 163 T; 3 other;

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Query Match 77.1%; Score 268.2; DB 21; Length 720;
Best Local Similarity 85.3%; Pred. No. 4.4e-73;
Matches 297; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCCCTGGAGAGCGGCGCTCC 60
DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTCCCTGGAGAGCGGCGCTCC 120
QY 61 ATCTCTGCTGCTGAGTGAAGTCTCTCTGTATAGGATGGGAAGACATATCTTGAATTGG 120
DB 121 ATCTCTGCTGAGGCTCTTCTCAGAGCTCTCTGATAGTAATGGAACAATATTTGGATTGG 180
QY 121 TACCTGCAGAGCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 181 TATCTGCAGAGCAGGCGAGTCTCTACAGCTCTCTGATCTATTGTTGGGCTNTATCGGGCC 240
QY 181 TCAGGGTCTCTGACAGTCTCAGTGGCAGTGGATGATCAGGACGACAGATTTTACACTGAAATC 240
DB 241 TCCGGGTCCTTCCAGCTTCTCAGTGGCAGTGGATGATCAGGACGACAGATTTTACACTGAAATC 300
QY 241 AGCAGCTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 301 AGCAGCTGAGGCTGAGAGTGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360
QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGCTACGGTGGCT 348
DB 361 TTCACTTTCGGCCCTGGACCAAGTGGATATCAACGAACTGTGGCT 408

RESULT 13
AAAL3929
ID AAAL3929 standard; DNA; 720 BP.
XX
XX AAAL3929;
XX
XX 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 5B12-16-12 DNA SEQ ID NO:21.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
XX Homo sapiens.
XX
XX JF2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NIBS ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX
XX P-PSDB; AAY82619.
XX
XX A human monoclonal antibody to parathyroid hormone related protein,
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Example 10; Page 57-58; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone nucleotide sequence from the
XX present invention.
XX
XX Sequence 720 BP; 174 A; 193 C; 187 G; 163 T; 3 other;

```

CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 169 A; 189 C; 190 G; 157 T; 15 other;

Query Match 77.0%; Score 267.8; DB 21; Length 720;
 Best Local Similarity 85.1%; Pred. No. 5.8e-73;
 Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACCTCAGCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 60
 DB 61 GATATTGTGATGANTCAGTNTCCACTNNCTCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 120
 QY 61 ATCTCTCTGCTGCTGAGTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 DB 121 ATCTCTCTGCTGCTGAGTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 180
 QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCGCGGCA 180
 DB 181 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTCTGATCGGCC 240
 QY 181 TCAGGGGTCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240
 DB 241 TCCGGGGTCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTCAGGTTGCGCCAGGACCAAGCTGGAGATCAAAACGTTACGGTGGCT 348
 DB 361 TTCAGTTCGGCCCTGGAGACCAAGTGGATATCAAAACGAACTGTGGCT 408

RESULT 14

AA13922

ID AA13922 standard; DNA; 720 BP.

XX AC AA13922;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone IB3-9-16 DNA SEQ ID NO:7.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;

XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;

XX fracture; cachexia; tooth disease; periodontal disease; gingiva;

XX sepsis; systemic inflammatory response syndrome; SIRS;

XX hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.

XX Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX 17-JUN-1998; 98JP-0188196.

XX 26-JUN-1998; 98JP-0196729.

XX (NISE) JAPAN TOBACCO INC.

XX WPI: 2000-286723/25.

XX P-PSDB; AAY82612.

XX A human monoclonal antibody to parathyroid hormone related protein.

PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain

XX Example 10; Page 36-37; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 174 A; 190 C; 187 G; 166 T; 3 other;

Query Match 76.6%; Score 266.6; DB 21; Length 720;

Best Local Similarity 85.1%; Pred. No. 1.4e-72;

Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACCTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 60
 DB 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 120
 QY 61 ATCTCTCTGCTGCTGAGTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 DB 121 ATCTCTCTGCTGCTGAGTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 180
 QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCGCGGCA 180
 DB 181 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCGCGGCA 240
 QY 181 TCAGGGGTCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240
 DB 241 TCCGGGGTCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTCAGGTTGCGCCAGGACCAAGCTGGAGATCAAAACGTTACGGTGGCT 348
 DB 361 TTCAGTTCGGCCCTGGAGACCAAGTGGATATCAAAACGAACTGTGGCT 408

RESULT 15

AAF44895

ID AAF44895 standard; cDNA; 963 BP.

XX AC AAF44895;

XX 28-MAR-2001 (first entry)

XX Human breast cancer related protein coding sequence SEQ ID NO: 51.

XX Human; breast cancer; diagnosis; therapy; vaccine; ss.

XX Homo sapiens.

XX WO200078960-A2.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17536.

XX 23-JUN-1999; 99US-0140903.

XX 12-OCT-1999; 99US-0158980.

PA (CORI-) CORIXA CORP.
XX
PI Yuqiu J, Mitcham JL;
XX
DR WPI; 2001-041426/05.
XX
PT New polynucleotides encoding breast tumor specific proteins, useful for
PT prevention, treatment and diagnosis of breast cancer -
XX
PS Claim 25; Page 135-136; 165pp; English.
XX
CC The present invention provides the coding sequences for a number of
CC breast cancer related proteins. These can be used in vaccinations
CC against, diagnosis of and treatment of cancer, particularly breast
CC cancer.
XX
SQ Sequence 963 BP; 253 A; 264 C; 224 G; 213 T; 9 other;
Query Match 75.68; Score 263.2; DB 22; Length 963;
Best Local Similarity 84.84; Pred. No. 1.7e-71;
Matches 295; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCCGCCCTCC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
63 GATATTGTGATGACTCAGTCTCCACTCTCCAGCGCGTCACCCCTGGAGAGCCGCCCTCC 122
QY 61 ATCTCTGTGCGTCCAGTAAAGTCTCTGTATANGGNTGGGAAGACATCTTGAATTGG 120
Db |||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
123 ATCTCTGCAAGTCTAGTCAGAGCTCTACATAGTAGTAATGGATACAGTTATTGGATTGG 182
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
183 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGCTTTCTAAGCGGGCC 242
QY 181 TCAGGGGTCCTGTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
243 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 302
QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
303 AGTAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 362
QY 301 TTCAGGTCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
Db ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
363 CTCACCTTCGGCGGAGGACCAAGGTGGAGATCAAAACGAACCTGTGGCT 410

Search completed: April 26, 2003, 05:05:49
Job time : 74.0118 secs


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Db 559 TCCGGGTCCTGACAGGTTCCAGTGGCAGTGTATCAGGCACAGATTTTACACTGAGAAATC 618
Qy 241 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 619 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGGCTTACAGAGTCCA 678
Qy 301 TTCAGTTTCGCCCAAGGACCAAGGTGGAGATCAAACTAGGG 343
Db 679 TTCACCTTTCGGCCCTGGGACCAAGTGGATATCAACAGAGGG 721

RESULT 2
US-09-822-698A-2
; Sequence 2, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 2
; LENGTH: 339
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
; US-09-822-698A-2

Query Match 75.5%; Score 262.8; DB 10; Length 339;
Best Local Similarity 86.1%; Pred. No. 2.1e-78; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 47;

Qy 1 GATATTGTGATGACTGACTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCGCTCC 60
Db 1 GAAATTGTGCTGACTGACTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCGCTCC 60
Qy 61 ATCTCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 61 ATCTCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATATTTGATGTCACCCGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATATTTGATGTCACCCGGCC 180
Qy 181 TCAGGGTTCCTGACAGTTCCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 181 TCCGGGTTCCTGACAGTTCCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Qy 241 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Qy 301 TTCAGTTTCGCCCAAGGACCAAGGTGGAGATCAAAAGC 338
Db 301 TTCACCTTTCGGCCCTGGGACCAAGTGGATATCAACAG 338

RESULT 3
US-09-822-698A-25
; Sequence 25, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
```

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; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 25
; LENGTH: 663
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
; US-09-822-698A-25

Query Match 75.5%; Score 262.8; DB 10; Length 663;
Best Local Similarity 86.1%; Pred. No. 2.7e-78; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 47;

Qy 1 GATATTGTGATGACTGACTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCGCTCC 60
Db 1 GAAATTGTGCTGACTGACTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCGCTCC 60
Qy 61 ATCTCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 61 ATCTCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATATTTGATGTCACCCGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATATTTGATGTCACCCGGCC 180
Qy 181 TCAGGGTTCCTGACAGTTCCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db 181 TCCGGGTTCCTGACAGTTCCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Qy 241 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Qy 301 TTCACCTTTCGGCCCTGGGACCAAGTGGAGATCAAAAGC 338
Db 301 TTCACCTTTCGGCCCTGGGACCAAGTGGAGATCAAAAGC 338

RESULT 4
US-09-924-340-7
; Sequence 7, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
```


LOCATION: 32...748
NAME/KEY: 3'UTR
LOCATION: 749...968
NAME/KEY: polyA_signal
LOCATION: 928...933
NAME/KEY: polyA_site
LOCATION: 953...968
US-09-924-340-7

Query Match 73.8%; Score 256.8; DB 9; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-76;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 60
DB 92 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 151
QY 61 ATCTCCTGTGCGTCGAGTAAGAGTCTCCTGTATAGGATGGGAACATATCTTGAATTGG 120
DB 152 ATCTCCTGTGCGTCGAGTCAGAGCCTCTCGATGTTCAAGGCTCCAACTATTGGATTGG 211
QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
DB 212 TACCACCAAGAGCCAGGCGAGTCTCCAACTCCTGATATATCTTGGGTTCTTAATCGGGCC 271
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 272 TCCGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 331
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 332 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCA 391
QY 301 TTCAGGTTCCGCCAAGGACCAAGTGGAGATCAAACTGAGTGGCT 348
DB 392 TTCAGTTCGGCCCTGGGACCAAGTGGATATCAAGCAAGTGGCT 439

RESULT 5

US-09-992-600A-7
Sequence 7, Application US/09992600A
Publication No. US20030027161A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
SEQ ID NO 7
LENGTH: 968
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1...31
FEATURE:
NAME/KEY: CDS
LOCATION: 32...748

FEATURE:
NAME/KEY: 3'UTR
LOCATION: 749...968
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 928...933
FEATURE:
NAME/KEY: polyA_site
LOCATION: 953...968
US-09-992-600A-7

Query Match 73.8%; Score 256.8; DB 9; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-76;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 60
DB 92 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCC 151
QY 61 ATCTCCTGTGCGTCGAGTAAGAGTCTCCTGTATAGGATGGGAAGACATATCTTGAATTGG 120
DB 152 ATCTCCTGTGCGTCGAGTCTAGTCAGAGCCTCCTGATGTTCAAGGCTCCAACTATTGGATTGG 211
QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
DB 212 TACCACCAAGAGCCAGGCGAGTCTCCAACTCCTGATATATCTTGGGTTCTTAATCGGGCC 271
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 272 TCCGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 331
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 332 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCA 391
QY 301 TTCAGGTTCCGCCAAGGACCAAGTGGAGATCAAACTGAGTGGCT 348
DB 392 TTCAGTTCGGCCCTGGGACCAAGTGGATATCAAGCAAGTGGCT 439

RESULT 6

US-09-848-798-99
Sequence 99, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 99
LENGTH: 336
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain G01
US-09-848-798-99

Query Match 72.4%; Score 252; DB 9; Length 336;
Best Local Similarity 84.9%; Pred. No. 9e-75;
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 7 GTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCCATCTCC 66
DB 4 GAGCTCACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCTCCATCTCC 63

```
Qy 67 TGTCTGCTGAGTAAAGTCTCTCTATAGAGTAGGGAGACATACCTTGAATTGGTACCTG 126
Db 64 TGCAGGTCTAGTACAGAGCTCTCATAGTAGTGATCACTTTTGGATTGGTACCTG 123
Qy 127 CAGAAGCCAGGCGAGTCCACAGCTCTCTGATCTATTTGATGTCCACCGGCGATCAGG 186
Db 124 CAGAAGCCAGGCGAGTCCACAGCTCTCTGATCTATATGTTTAAATCGGCGCTCCGG 183
Qy 187 GTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGCAGA 246
Db 184 GTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGCAGA 243
Qy 247 GTGAGGCTGAGGATGTGGGTTTATTACTGTCAACAGCTGTAGAGTATCCATTCACG 306
Db 244 GTGAGGCTGAGGATGTGGGTTTATTACTGTCAACAGCTGTAGAGTATCCATTCACCT 303
Qy 307 TTCGGCCAAAGGACCAAGGTGGAGATCAAAACG 338
Db 304 TTCGGCCGAGGACCAAGGTGGAGATCAAAACG 335

RESULT 7
US-10-158-646-61
; Sequence 61, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329931.2
US-10-158-646-61

Query Match 71.9%; Score 250.2; DB 9; Length 738;
Best Local Similarity 84.0%; Pred. No. 4.7e-74;
Matches 295; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCGCTCC 60
Db 81 GATATTGTGATGACCCAGACTCCAGCTCCCTGCCGTCACCCCTCGAGAGCGGCGCTCC 140
Qy 61 ATCTCTGTCTCGTAGTAGTCTCTGTATATA---AGATGGGAAGACATACCTTGAAT 117
Db 141 ATCTCTGTGAGGCTAGTCAGAGCTCTCTGATAGTATGATGAAACACCTATTGTGGAC 200
Qy 118 TGGTACCTGCAGAGCAGGAGGAGTCTCCACAGCTCTGATCTATTGATGTCACCCGG 177
Db 201 TGGTACCTGCAGAGCAGGAGGAGTCTCCACAGCTCTGATCTATTGATGTCACCCGG 260
Qy 178 GCATCAGGGTCTCCAGAGGTTTCAGTGGCAGTGGATCAGGCACACATTTTACACTGAA 237
Db 261 GCCTCTGAGTCCACAGAGGTTTCAGTGGCAGTGGATCAGGCACACTAATTTACACTGAA 320
Qy 238 ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTAGAGTAT 297
Db 321 ATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTAGAGTAT 380
Qy 298 CCATTACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGATACGTTGCGCT 348
Db 381 CCGTCTACTTTCCGCGAGGACCAAGGTAGAGATCAAAACGATACGTTGCGCT 431
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RESULT 8
US-09-864-761-32306
; Sequence 32306, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32306
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001224.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
; OTHER INFORMATION: EST_HUMAN HIT: AA464313.1, EVALUOE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P06309, EVALUOE 9.00e-55
; OTHER INFORMATION: NT HIT: X12691.1, EVALUOE 0.00e+00
US-09-864-761-32306

Query Match 69.4%; Score 241.4; DB 10; Length 476;
Best Local Similarity 85.4%; Pred. No. 3.7e-71;
Matches 269; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCGCTCC 60
Db 12 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCGCTCC 71
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QY 61 ATCTCTGTCGCTGAGTAAGACTCTCTGTATTAAGGATGGAGACACATACCTGAATTGG 120
DB 72 ATCTCTGTCGAGTCTAGTCAGAGCCCTCTGCATAGTAATGGATACAACTATTGGATTGG 131
QY 121 TACCTGAGAAAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTGATCTCCACCCGGGCA 180
DB 132 TACCTGAGAAAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTGGTCTTAATCGGGCC 191
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 192 TCCGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 251
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 252 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTACAACTCCT 311
QY 301 TTCAGGTTCCGCCAA 315
DB 312 CCCACAGTGGGTACAA 326
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RESULT 9

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US-09-864-761-15798
; Sequence 15798, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Asomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIORITY FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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; SOFTWARE: Rnobox Sequence Listing Engine vers. 1.1
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; SEQ ID NO 15798
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001224.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
US-09-864-761-15798
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Query Match 59.4%; Score 241.4; DB 10; Length 563;
Best Local Similarity 85.4%; Pred. No. 3.9e-71;
Matches 269; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGAGAGCGCGCTCC 60
DB 62 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGAGAGCGCGCTCC 121
QY 61 ATCTCTGTCGCTGAGTGAAGTCTCTGTATTAAGGATGGAGACATACCTGAATTGG 120
DB 122 ATCTCTGTCAGGCTAGTCAGAGCCCTCTCATAGTAATGGATACAACTATTGGATTGG 181
QY 121 TACCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCGGGCA 180
DB 182 TACCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTGGTCTTAATCGGGCC 241
QY 181 TCAGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 242 TCCGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 301
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 302 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTACAACTCCT 361
QY 301 TTCAGGTTCCGCCAA 315
DB 362 CCCACAGTGGGTACAA 376
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RESULT 10

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US-09-479-614-25
; Sequence 25, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-25
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Query Match 68.7%; Score 239.2; DB 9; Length 666;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGATCGCAGAGCCCTCTCTGTCCTGTCCTGTCAGAGCGAGCGCTCA 60
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAGAGTGGAGAGACATACCTGAATTGG 120
DB 61 ATCTCTGTCAGGGCCAGTGTACAGCTCTCTGTACAGTGTGAGAAATACCTTATCTGAATTGG 120
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QY 121 TACCTGCAGAGCCAGCGGACAGTCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 121 TACCTGCAGAGCCAGCGGACAGTCTCCACAGAGCTCCTGATCTATTGTTTCCAAACCGGAC 180
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
Db 181 TCTGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
QY 241 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCAGTTTCGCCCAAGGACCAAGGTTGGAGATCAAAACGTTACGGTGGCT 348
Db 301 CTCACCTTCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGATGCT 348

RESULT 11

US-09-479-614-27/c
; Sequence 27, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-27

Query Match 68.7%; Score 239.2; DB 9; Length 666;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCCGGCCTCC 60
Db 666 GATATTGTGATGAGCAGACACCCCTCTGCTCCCTGCTCCCTGGAGAGCCAGCCTCA 607
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGATAGGATGGAGACACATCTTGAATTGG 120
Db 606 ATCTCTCTGAGGCGCAGTCAAGCCCTCTGTCAGTGTGAGGATGATCTTCTGAATTGG 547
QY 121 TACCTGCAGAGCCAGCGGACAGTCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 546 TACCTGCAGAGCCAGCGGACAGTCTCCACAGGCTTGTATCTATTGTTTCCAAACCGGAC 487
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
Db 486 TCTGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 427
QY 241 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 426 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCAGTTTCGCCCAAGGACCAAGGTTGGAGATCAAAACGTTACGGTGGCT 348
Db 366 CTCACCTTCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGATGCT 319

RESULT 12

US-09-479-614-23
; Sequence 23, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-23

Query Match 68.7%; Score 239.2; DB 9; Length 726;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCCGGCCTCC 60
Db 61 GATATTGTGATGAGCAGACCCCTCTGCTCCCTGCTCCCTGGAGAGCCAGCCTCA 120
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTCTGTATAAGGATGGAGACATCTTGAATTGG 120
Db 121 ATCTCTCTGAGGCGCAGTCAGAGCCTCTGTACAGTGTAGGAAATCTTATCTGAATTGG 180
QY 121 TACCTGCAGAGCCAGCGGACAGTCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 181 TACCTGCAGAGCCAGCGGACAGTCTCCACGGCGTTGATCTATCTGTTCCAAACCGGAC 240
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
Db 241 TCTGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 300
QY 241 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 301 ACCAGATGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 348
QY 301 TTCAGTTTCGCCCAAGGACCAAGGTTGGAGATCAAAACGTTACGGTGGCT 348
Db 361 CTCACCTTCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGATGCT 408

RESULT 13

US-09-479-614-24/c
; Sequence 24, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-24

Query Match 68.7%; Score 239.2; DB 9; Length 726;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCCCTGGAGAGCCGGCCTCC 60
Db 666 GATATTGTGATGAGCAGACCCCTCTGCTCCCTGCTCCCTGGAGAGCCAGCCTCA 607

1

QY 61 ATCTCTCTCTCGCTCGAGTATAGAGTCTCTCTGTATATAAGATGGGAAGACATCTTGAATTGG 120
DB 606 ATCTCTCTCGAGGCGAGTCTGACAGCTCTCTGTACAGTGTGGAATCTATCTGAATTGG 547
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATTTGATGTCCACCCGGGCA 180
DB 546 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATCTTGTTCACACCGGGAC 487
QY 181 TCAGGGGTCCCTGCAGAGTTCAGTGGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 486 TCTGGGGTCCACAGAGTTCAGTGGGAGTGGGTCAGGCACAGATTTTACACTGAAATC 427
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
DB 426 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTGGTCAAGGTTTACAGCATCT 367
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
DB 366 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 319

RESULT 14
US-09-479-614-19
; Sequence 19, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Fells catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(732)
; FEATURE:
US-09-479-614-19

Query Match 68.7%; Score 239.2; DB 9; Length 954;
Best Local Similarity 80.5%; Pred. No. 2.5e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGAGAGCGGCTCC 60
DB 67 GATATTGTGATGACCGACAGCCCTCTGTCCCTGTCCCTGACCCCTGAGAGCGGCTCA 126
QY 61 ATCTCTCTCTCGCTCGAGTATAGAGTCTCTCTGTATATAAGATGGGAAGACATCTTGAATTGG 120
DB 127 ATCTCTCTCGAGGCGAGTCTCTGTACAGTGTGGAATCTATCTGAATTGG 186
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATTTGATGTCCACCCGGGCA 180
DB 187 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATCTTGTTCACACCGGGAC 246
QY 181 TCAGGGGTCCCTGCAGAGTTCAGTGGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 247 TCTGGGGTCCACAGAGTTCAGTGGGAGTGGGTCAGGCACAGATTTTACACTGAAATC 306
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
DB 307 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTGGTCAAGGTTTACAGCATCT 366
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
DB 367 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 414

RESULT 15
US-09-479-614-21/c
; Sequence 21, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Fells catus
US-09-479-614-21

Query Match 68.7%; Score 239.2; DB 9; Length 954;
Best Local Similarity 80.5%; Pred. No. 2.5e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGAGAGCGGCTCC 60
DB 888 GATATTGTGATGACCGACAGCCCTCTGTCCCTGTCCCTGACCCCTGAGAGCGGCTCA 829
QY 61 ATCTCTCTCTCGCTCGAGTATAGAGTCTCTCTGTATATAAGATGGGAAGACATCTTGAATTGG 120
DB 828 ATCTCTCTCGAGGCGAGTCTCTGTACAGTGTGGAATCTATCTGAATTGG 769
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATTTGATGTCCACCCGGGCA 180
DB 768 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTCATCTATCTTGTTCACACCGGGAC 709
QY 181 TCAGGGGTCCCTGCAGAGTTCAGTGGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 708 TCTGGGGTCCACAGAGTTCAGTGGGAGTGGGTCAGGCACAGATTTTACACTGAAATC 649
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
DB 648 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTGGTCAAGGTTTACAGCATCT 589
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
DB 588 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 541

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Job time : 37.6331 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)

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Title: US-09-674-716B-17

Perfect score: 348

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	261.2	75.1	339	1 US-08-082-623-2	Sequence 2, Appli
2	252.8	72.6	336	3 US-09-000-088-1	Sequence 1, Appli
3	252.8	72.4	336	4 US-09-240-274-99	Sequence 99, Appl
4	249.4	71.7	339	1 US-08-264-093-9	Sequence 9, Appli
5	244	70.1	420	4 US-09-214-095D-111	Sequence 111, App
6	244	70.1	464	1 US-08-438-123-15	Sequence 15, Appl
7	243.6	70.0	339	2 US-08-672-345C-88	Sequence 88, Appl
8	243.6	70.0	339	4 US-09-214-095D-99	Sequence 99, Appl
9	240.4	69.1	368	2 US-08-672-345C-86	Sequence 86, Appl
10	240.4	69.1	368	4 US-09-214-095D-107	Sequence 107, App
11	239.2	68.7	368	2 US-08-672-345C-90	Sequence 90, Appl
12	239.2	68.7	368	4 US-09-214-095D-103	Sequence 103, App
13	238.8	68.6	339	4 US-09-406-532-13	Sequence 13, Appl
14	231.6	66.6	375	1 US-08-482-882-65	Sequence 65, Appl
15	231.6	66.6	375	1 US-08-483-389-65	Sequence 65, Appl
16	231.6	66.6	375	2 US-08-487-113D-65	Sequence 65, Appl
17	231.6	66.6	375	2 US-08-473-503-65	Sequence 65, Appl
18	231.6	66.6	375	2 US-08-483-932-65	Sequence 65, Appl
19	231.6	66.6	375	2 US-08-720-420A-65	Sequence 65, Appl
20	231.6	66.6	375	3 US-08-714-017-65	Sequence 65, Appl
21	231.6	66.6	375	3 US-08-475-680-65	Sequence 65, Appl
22	228.8	65.7	336	3 US-08-483-749A-3	Sequence 3, Appli
23	227.4	65.3	373	3 US-08-732-708C-40	Sequence 40, Appl
24	226	64.9	399	1 US-08-253-877C-9	Sequence 9, Appli
25	226	64.9	399	2 US-08-452-164A-9	Sequence 9, Appli
26	226	64.9	399	3 US-08-603-024-3	Sequence 3, Appli
27	225.2	64.7	882	1 US-08-392-419-3	Sequence 3, Appli

28 224.8 64.6 720 3 US-08-487-550-5 Sequence 5, Appli
29 222.2 63.9 1095 3 US-08-875-811-52 Sequence 52, Appl
30 222.2 63.9 1098 3 US-08-875-811-54 Sequence 54, Appl
31 221.2 63.6 405 1 US-08-259-372A-11 Sequence 11, Appl
32 221.2 63.6 405 1 US-08-468-671-11 Sequence 11, Appl
33 218.6 62.8 394 1 US-07-977-696C-64 Sequence 64, Appl
34 218.6 62.8 394 1 US-08-129-930B-64 Sequence 64, Appl
35 218.6 62.8 394 4 US-08-976-288A-64 Sequence 64, Appl
36 215.6 62.0 325 1 US-08-468-661-4 Sequence 4, Appli
37 215.6 62.0 325 1 US-08-466-272A-4 Sequence 4, Appli
38 215.6 62.0 325 1 US-08-478-857-4 Sequence 4, Appli
39 215.6 62.0 325 2 US-08-471-771-4 Sequence 4, Appli
40 215.6 62.0 325 3 US-09-130-783-4 Sequence 4, Appli
41 215.2 61.8 427 1 US-08-053-171-8 Sequence 8, Appli
42 214.2 61.6 749 4 US-08-983-035A-46 Sequence 46, Appl
43 214.2 61.6 1611 4 US-08-983-035A-37 Sequence 37, Appl
44 213.8 61.4 394 1 US-08-129-930B-93 Sequence 93, Appl
45 213.8 61.4 394 4 US-08-134-346A-48 Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-08-082-623-2
; Sequence 2, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..339
; OTHER INFORMATION: /standard_name= "Nucleotide
; OTHER INFORMATION: Sequence of the V-1 region of SDZ MSL 109"
; Patent No. 5750106

US-08-082-623-2

Query Match 75.1%; Score 261.2; DB 1; Length 339;
Best Local Similarity 85.8%; Pred. No. 6.6e-75;
Matches 290; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
Db 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
QY 61 ATCTCCTCTCGCTCGAGTAAGAGTCTCTGTATTAAGATGGAGACATACCTGAATTGG 120
Db 61 ATCTCCTCGAGTCTAGTCAGAGCTCTCTGCATACCTAATGGATACACTATTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTCTGGCTTCTAATCGGGC 180
QY 181 TCAGGGTCCCTGACAGCTTCAAGTGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 181 TCCGGGGTCCCTGACAGCTTCAAGTGGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTATGTCATGCAAGCTCTACAAATCCT 300
QY 301 TTCAGTTCGCCCAAGGACCAAGGTGGAGATCAACG 338
Db 301 CGGACGTTCCGCCAAGGACCAAGGTGGAAATCAACG 338

RESULT 2

US-09-000-088-1
; Sequence 1, Application US/09000088
; Patent No. 6146629
; GENERAL INFORMATION:
; APPLICANT: DAGAN, Shlomo
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST HEPATITIS B VIRUS
; TITLE OF INVENTION: SURFACE ANTIGEN (HBVSA9)
; FILE REFERENCE: DAGAN-1
; CURRENT APPLICATION NUMBER: US/09/000,088
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: PCT/IL97/00183
; EARLIER FILING DATE: 1997-06-10
; EARLIER APPLICATION NUMBER: IL96/118626
; EARLIER FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 336
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(336)
US-09-000-088-1

Query Match 72.6%; Score 252.8; DB 3; Length 336;
Best Local Similarity 84.5%; Pred. No. 3.4e-72;
Matches 284; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
Db 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
QY 61 ATCTCCTCTCGCTCGAGTAAGAGTCTCTGTATTAAGATGGAGACATACCTGAATTGG 120
Db 61 ATCTCCTCGAGGCTAGTCAGAGCTCTCTGCATAGTCTGGAAACACACTATTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTTGGTTCTAATCGGGC 180

QY 181 TCAGGGTCCCTGACAGTTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 181 TCCGGGTCCCTGACAGTTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGTACAAATCCT 300
QY 301 TTCACCTTCGGCCAAAGGACCAAGGTGGAGATCAAA 336
Db 301 CGGACTTTGGCCAGGGGACCAAGCTGGAGATCAAA 336

RESULT 3

US-09-240-274-99
; Sequence 99, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-99

Query Match 72.4%; Score 252; DB 4; Length 336;
Best Local Similarity 84.9%; Pred. No. 6.1e-72;
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 7 GTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCCATCTCC 66
Db 4 GAGCTCACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCCATCTCC 63
QY 67 TCTCCTCGAGTAAGAGTCTCTGTATTAAGATGGAGACATACCTTGAATTTGGTACCTG 126
Db 64 TCCAGGTCTAGTCAGAGCTCTCTGCATAGTAGTGATTCACATTTTGGATTGGTACCTG 123
QY 127 CAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCATCAGG 186
Db 124 CAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATATGGTTCTTAATCGGCCCTCCGG 183
QY 187 GTCCCTGACAGGTTTCAAGTGGAGTGGATCAGGCACAGATTTTACACTGAAATCAGAGA 246
Db 184 GTCCCTGACAGGTTTCAAGTGGAGTGGATCAGGCACAGATTTTACACTGAAATCAGAGA 243
QY 247 GTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCATTACG 306
Db 244 GTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCATTACG 303
QY 307 TTCGCCCAAGGACCAAGGTGGAGATCAACG 338
Db 304 TTCGCCGAGGACCAAGGTGGAGATCAACG 335

RESULT 4

US-08-264-093-9
; Sequence 9, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan

;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
;; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
;; TITLE OF INVENTION: ANTIGEN
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ridout & Maybee
;; STREET: 2300 Richmond-Ageleide Centre
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5H 2J7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: MS-DOS 6.00
;; SOFTWARE: ASCII Editor
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/264,093
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA: No. 5639863 applicable
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lake, James R.
;; REGISTRATION NUMBER: 31081
;; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 868-1482
;; TELEFAX: (416) 362-0823
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 339 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single stranded
;; TOPOLOGY: linear
;; US-08-264-093-9

Query Match 71.7%; Score 249.4; DB 1; Length 339;
Best Local Similarity 85.5%; Pred. No. 4.2e-71;
Matches 290; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGCTGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGACCCAGACTCCACTCTCCCTGCGGCTGAGAGCGCGCTCC 60
QY 61 ATCTCCTGCTCCAGTAAAGTCTCTGTATA--AGGATGGGAAGACATCTTGAAT 117
DB 61 ATCTCCTGCTCCAGTAAAGTCTCTGTATA--AGGATGGGAAGACATCTTGAAT 117
QY 118 TGGTACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGG 177
DB 121 TGGTACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGG 180
QY 178 GCATCAGGGTCCCTGACAGGTTGAGTGGCAGTGGATGAGCAGACAGATTTACACTGAAA 237
DB 181 GCCTGTGAGTCCAGAGGTTGAGTGGCAGTGGATGAGCAGACAGATTTACACTGAAA 240
QY 238 ATCAGCAGGTGGAGGCTGAGGATGTTGGGTTTATTACTTCAACAGCTGGTAGAGTAT 297
DB 241 ATCAGCAGGTGGAGGCTGAGGATGTTGGGTTTATTACTTCAACAGCTGGTAGAGTAT 300
QY 298 CAATTCAGTTCGGCAAGGACCAAGGTGGAGATCAAA 336
DB 301 CCTTTCACTTTCGGGGAGGACCAAGGTGGAGATCAAA 339

RESULT 5
US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

;; FILE REFERENCE: 51400-A-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/214,095D
;; CURRENT FILING DATE: 1999-07-19
;; NUMBER OF SEQ ID NOS: 121
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 111
;; LENGTH: 420
;; TYPE: DNA
;; ORGANISM: Murine
;; FEATURE:
;; NAME/KEY: V-segment
;; LOCATION: (1)..(403)
;; OTHER INFORMATION: n at any position represents any nucleotide including c.g.t.a,
US-09-214-095D-111

Query Match 70.1%; Score 244; DB 4; Length 420;
Best Local Similarity 81.3%; Pred. No. 2.5e-69;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGCTGAGAGCGCGCTCC 60
DB 53 GATATTGTGATGACCGCAGGATCACTCCAATCCTGTCACTTCTGGAGATCAGTTTCC 112
QY 61 ATCTCCTGCTCCAGTAAAGTCTCTGTATAAGGATGGAGACATCTTGAATTGG 120
DB 113 ATCTCCTGCTCCAGTAAAGTCTCTGTATAAGGATGGAGACATCTTGAATTGG 172
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATCTCCACCGGGCA 180
DB 173 TTTCTGCGAGACAGGAGGATCTCCTCACTCTCTGATCTATTGATCTCCACCGGTGCA 232
QY 181 TCAGGGGTCCCTGACAGGTTTCACTGCGAGTGGATGAGCAGGACAGATTTACACTGAAAAATC 240
DB 233 TCAGGAGTCTCAGACCGGTTTGTAGTGGTCTCAGGACAGATTTACCTCGGAAATC 292
QY 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTTCAACAGCTGGTAGATATCCA 300
DB 293 AGTAGAGTGAAGGCTGAGGATGTTGGGTTTATTACTTCAACAGCTGGTAGATATCCA 352
QY 301 TTCACCTTCGGCCAGGACCAAGGTGGAGATCAAAACGTACCGTGGCT 348
DB 353 TTCACCTTCGGCTCGGACCAAGGTGGAGATCAAAACGTGGATGCT 400

RESULT 6
US-08-438-123-15
; Sequence 15, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins

REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 base pairs
TYPE: Nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-438-123-15

Query Match 70.1%; Score 244; DB 1; Length 464;
Best Local Similarity 81.3%; Pred. No. 2.6e-69;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 102 GATATTGTGATGACTCCAGTCTCCAGTCTCCCTGACCTCTGACCTCTCTGGAGAGTCACTATCC 161
QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGATATAGGATGGGAACACATCTTGAATTGG 120
DB 162 ATCTCTGTCAGGCTAGTAAAGTCTCTCTGATATAGGATGGGAACACATCTTGAATTGG 221
QY 121 TACCTGCAGAAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 222 TTCTCTGAGAGGCGAGGCTCTCTGATATAGGATGGGAACACATCTTGAATTGG 281
QY 181 TCAGGGTCTCTGACAGTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 240
DB 282 TCAGGAGTCCGACAGAGTTCAGTGGCAGTGGATGAGCAGACAGTTCCTTACACTGAAATC 341
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 342 AGTAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCTGCAACATCTAGAGTATCCG 401
QY 301 TTCACGTTCCGCAAGGCGAGGTCGAGATCAACGTCACGGTGGCT 348
DB 402 TTCACGTTCCGCTCTGGGACCAAGCTGGAGCTGAAACGGGTGATGCT 449

RESULT 7

US-08-672-345C-88
Sequence 88, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:

APPLICANT: Landry Donald, W.

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672.345C

FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-672-345C-88

Query Match 70.0%; Score 243.6; DB 2; Length 339;

Best Local Similarity 82.5%; Pred. No. 3.1e-69;

Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGACCTCTGCAATCTCTGGAGATCACTATTTCC 60
QY 61 ATCTCTGTCGCTCGASTAAGAGTCTCTCTGTATAAGGATGGGAACACATCTTGAATTGG 120
DB 61 ATCTCTGTCAGGCTAGTAGGAGTCTCTCTATATAGGATGGGAACACATCTTGAATTGG 120
QY 121 TACCTGCAGAAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 121 TTCTCTGAGAGGCGAGGCTCTCTCAACTCTCTGATCTATTGATGTCACCCGGTTC 180
QY 181 TCAGGGTCTCTGACAGTTCAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 240
DB 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGAACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGTAGAGTGAAGGTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCACGTTCCGCAAGGCGAGGTCGAGATCAACGTCACGGTGGCT 338
DB 301 TTCACGTTCCGCTCTGGGACCAAGTTCGAGATCAACG 338

RESULT 8

US-09-214-095D-99

Sequence 99, Application US/09214095D

Patent No. 6280987

GENERAL INFORMATION:

APPLICANT: Landry, Donald

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

FILE REFERENCE: 51400-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/214,095D

NUMBER OF SEQ ID NOS: 121

SOFTWARE: Patent in version 3.0

SEQ ID NO 99

LENGTH: 339

TYPE: DNA

ORGANISM: Murine

US-09-214-095D-99

Query Match 70.0%; Score 243.6; DB 4; Length 339;

Best Local Similarity 82.5%; Pred. No. 3.1e-69;

Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGACCTCTGCAATCTCTGGAGATCACTATTTCC 60
QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTCTGTATAAGGATGGGAACACATCTTGAATTGG 120
DB 61 ATCTCTGTCAGGCTAGTAGGAGTCTCTCTATATAGGATGGGAACACATCTTGAATTGG 120
QY 121 TACCTGCAGAAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 121 TTCTCTGAGAGGCGAGGCTCTCTCAACTCTCTGATCTATTGATGTCACCCGGTTC 180
QY 181 TCAGGGTCTCTGACAGGTTTACAGTGGCAGTGGATGAGCAGACAGATTTTACACTGAAATC 240

Db 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTGAGGACAGATTTACCCCTGGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGTAGAGTGAAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTTTGTAGACTATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAACG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAGATAAAACG 338

RESULT 9

US-08-672-345C-86
; Sequence 86 Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 86:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 368 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-08-672-345C-86

Query Match 69.1%; Score 240.4; DB 2; Length 368;
Best Local Similarity 82.0%; Pred. No. 3.4e-68;
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATCACTCACTCTCCCTGCGCGTCCACCCCTGGAGAGCGCGCTCC 60
Db 1 GATATGGTGTGATGACGCAAGCAACTCTCCAATCCTGTCACTTCTGGAGAAATCACTTCC 60
QY 61 ATCTCCTGCTGCTGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120
Db 61 ATCTCCTGCTGCTGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120
QY 121 TACCTGCAAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTTGATGTCACCCGGGCA 180
Db 121 TTTCTGCAAGACAGGCAATCTCTCACCHCTGATCTATTTGATGTCACCCGGTCA 180
QY 181 TCAGGGGTCCTGACAGCTTCACTGAGTGGGAGTGGATGAGGACAGATTTTACACTGAAATC 240
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTACCCCTGGAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 241 AGTAGAGTGAAGGCTGAGGATGTTGGGTCGCTATTACTGTCAACAATTTGTAGATATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAACG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAAATAAGACG 338

RESULT 10

US-09-214-095D-107
; Sequence 107 Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 107

; LENGTH: 368

; TYPE: DNA

; ORGANISM: Murine

US-09-214-095D-107

Query Match 69.1%; Score 240.4; DB 4; Length 368;
Best Local Similarity 82.0%; Pred. No. 3.4e-68;
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATCACTCACTCTCCCTGCGCGTCCACCCCTGGAGAGCGCGCTCC 60

Db 1 GATATGGTGTGATGACGCAAGCAACTCTCCAATCCTGTCACTTCTGGAGAAATCACTTCC 60

QY 61 ATCTCCTGCTGCTGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120

Db 61 ATCTCCTGCTGCTGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120

QY 121 TACCTGCAAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTTGATGTCACCCGGGCA 180

Db 121 TTTCTGCAAGACAGGCAATCTCTCACCHCTGATCTATTTGATGTCACCCGGTCA 180

QY 181 TCAGGGGTCCTGACAGCTTCACTGAGTGGGAGTGGATGAGGACAGATTTTACACTGAAATC 240

Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTACCCCTGGAATC 240

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 241 AGTAGAGTGAAGGCTGAGGATGTTGGGTCGCTATTACTGTCAACAATTTGTAGATATCCA 300

QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAACG 338

Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAAATAAGACG 338

RESULT 11

US-08-672-345C-90
; Sequence 90, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:

; APPLICANT: Landry Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-672-345C-90

Query Match 68.7%; Score 239.2; DB 2; Length 368;
Best Local Similarity 80.5%; Pred. No. 8.3e-68;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTGAGAGCCGCGCTCC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
Db 1 GATATGGTATGCGCAAGATGAATCTCCAATCTCTGTCACCTTCTGGAGAAATCAGTTTC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
QY 61 ATCTCTCTGCTGAGTAAGAGTCTCTGTATATAAGGATGGAGACATCTTGAATTGG 120
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
Db 61 ATCTCTGAGGTCTAGTAGGAGTCTCTATATAGGATGGAGACATCTTGAATTGG 120
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QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGATCTCAACCTGAAATC 180
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Db 121 TTCTCTCAGAGCCAGGAGGAGTCTCTCACTCTCTGATCTATTGATCTCAACCTGAAATC 180
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QY 181 TCAGGGTCCCTGACAGGTTTCACTGAGTGGAGTCAACAGCTGATCAACCTGAAATC 240
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Db 181 TCAGGGTCCCTGACAGGTTTCACTGAGTGGAGTCAACAGCTGATCAACCTGAAATC 240
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QY 241 AGCAGAGTGGAGCTGAGGATCTGGGTTTATTACTGCAACAGCTGATGAGTATCCA 300
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Db 241 AGTAGAGTGAAGCTGAGGATCTGGGTTTATTACTGCAACAGCTGATGAGTATCCA 300
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QY 301 TTCACGTTCCGGCCAGGGACCAAGGTGGAGATCAACCTGAGTGGCT 348
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Db 301 TTCACGTTCCGGCCAGGGACCAAGGTGGAGATCAACCTGAGTGGCT 348
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RESULT 12
US-09-214-095D-103
; Sequence 103, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 368
; TYPE: DNA
; ORGANISM: MURINE
US-09-214-095D-103

Query Match 68.7%; Score 239.2; DB 4; Length 368;
Best Local Similarity 80.5%; Pred. No. 8.3e-68;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTGAGAGCCGCGCTCC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
Db 1 GATATGGTATGACGCAAGATGAATCTCCAATCTCTGTCACCTTCTGGAGAAATCAGTTTC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
QY 61 ATCTCTCTGCTGAGTAAGAGTCTCTGTATATAAGGATGGAGACATCTTGAATTGG 120
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Db 61 ATCTCTCTGAGTCTAGTAGGAGTCTCTATATAGGATGGAGACATCTTGAATTGG 120
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QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGATCTCAACCTGAAATC 180
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Db 121 TTCTCTCAGAGCCAGGAGGAGTCTCTCACTCTCTGATCTATTGATCTCAACCTGAAATC 180
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QY 181 TCAGGGTCCCTGACAGGTTTCACTGAGTGGAGTCAACAGCTGATCAACCTGAAATC 240
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Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTCAAGAACAGATTTCAACCTGAAATC 240
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QY 241 AGCAGAGTGGAGCTGAGGATCTGGGTTTATTACTGCAACAGCTGATGAGTATCCA 300
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Db 241 AGTAGAGTGAAGCTGAGGATCTGGGTTTATTACTGCAACAGCTGATGAGTATCCA 300
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QY 301 TTCACGTTCCGGCCAGGGACCAAGGTGGAGATCAACCTGAGTGGCT 348
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Db 301 TTCACGTTCCGGCCAGGGACCAAGGTGGAGATCAACCTGAGTGGCT 348
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RESULT 13
US-09-406-532-13
; Sequence 13, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(339)
; OTHER INFORMATION: 13H10 light chain v region
US-09-406-532-13

Query Match 68.6%; Score 238.8; DB 4; Length 339;
Best Local Similarity 81.7%; Pred. No. 1.1e-67;
Matches 276; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTGAGAGCCGCGCTCC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
Db 1 GATATCGTATGACTCAGGCTCGACTCTCTGTACCTGTCACCTCTGGAGAGTCAAGTATCC 60
||||| ||||||| || ||||||| || ||||||| || ||||||| || |||||
QY 61 ATCTCTCTGCTGAGTAAGAGTCTCTGTATATAAGGATGGAGACATCTTGAATTGG 120
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Db 61 ATCTCTGCAAGTCAAGTAGTAGTCTCTGTCATAGAAATGGCAACACTTACTTGTATTTGG 120
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QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGATCTCAACCTGAAATC 180
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Db 121 TTCTCTCAGAGCCAGGAGGAGTCTCTCAGCTCTCTGATATATATCGATCTCAACCTTGGC 180
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QY 181 TCAGGGTCCCTGACAGGTTTCACTGAGTGGAGTCAAGCAGATTTTACACTGAAATC 240
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Db 181 TCAGGAGTCCCAAGACAGGTTTCACTGAGTGGGTCAGGAACCTGCTTTCCACTGAGAAATC 240
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QY 241 AGCAGAGTGGAGCTGAGGATCTGGGTTTATTACTGCAACAGCTGATGAGTATCCA 300
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Db 241 ACTAGAGTGGAGGCTGAGGATGGGTGTTTATTACTGTATGCAACGCTGAGATATCCT 300
QY 301 TTCACGCTTCGGCAAGGACCAAGGTGGAGATCAAAACG 338
Db 301 TTCACGCTTCGGAGGGGGACCAAGCTGGAATAAAACG 338

RESULT 14
US-08-482-882-65
; Sequence 65, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,882
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773218and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-882-65

Query Match 66.6%; Score 231.6; DB 1; Length 375;
Best Local Similarity 79.8%; Pred. No. 2.3e-65;
Matches 273; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 GATATTGTGACACTCTCCACTCTCCCTGCCCCGCTGAGAGCGCGGCTCC 60
Db 22 GACATTGTAATGACCCAGCTCCACTCTCCCTGCTGTCTCTCTGGAGCGCCCTCC 81

QY 61 ATCTCCTGCTCGAGTAAGAGTCTCCTGTATTAAGGATGGAGACATACCTTGAATTGG 120
Db 82 ATCTCTTCGAGATCTAGTCAGAGCCTTGTACACAGTAAATGGAGACACCTATTACATTTG 141
QY 121 TACCTGCAGAGCCAGGCGCAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGCA 180
Db 142 TACCTGCAGAGCCAGGCGCAGTCTCCACAGCTCCTGATCTACAAAGTTTCCAAACCGATT 201
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 202 TCTGGGTCCCGACAGAGGTTTCACTGGCAGTGGATCAGGCAGAGATTTTACACTCAAGATC 261
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 262 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCTCAAGTACACATGTTCCG 321
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACGTACG 342
Db 322 TACACGTTCCGACAGGCGCAGGTCAGGTGGAATAAAACGTAAG 363

RESULT 15
US-08-483-389-65
; Sequence 65, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-RELATED PROTEIN
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,389
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sub, Young J.
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32760
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-483-389-65

Query Match 66.6%; Score 231.6; DB 1; Length 375;
Best Local Similarity 79.8%; Pred. No. 2.3e-65;
Matches 273; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy	1	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTCGAGAGCGGCCCTCC	60
Db	22	GACATTGTATGACCCAGTCTCCACTCTCCCTGCCCTCAGTCTCCCTCGAGAGCGGCCCTCC	81
Qy	61	ATCTCCTGTCTCGCTCGAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG	120
Db	82	ATCTCTTGACAGTCTAGTCAGAGCCTTGTACACAGTAATGGAGACACCTATTACATTGG	141
Qy	121	TACCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTGTGATGTCCACCCCGGCCA	180
Db	142	TACCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCCTGATCTACAAAGTTTCCAAACCGATTT	201
Qy	181	TCAGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC	240
Db	202	TCTGGGTCCCGACAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC	261
Qy	241	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	262	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCTCAAAAGTACACATGTTTCOG	321
Qy	301	TTCAGGTTCCGCCAAGGGACCAAGGTGGAGATCAACGTACG	342
Db	322	TACAGTTCGGACAGGGGACCAAGGTGGAAATAAACGTAAG	363

Search completed: April 26, 2003, 07:28:37
Job time : 15.4142 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 2664.21 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgggtgagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

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14: gb_vl:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

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21: em_or:**

22: em_ov:**

23: em_pat:**

24: em_ph:**

25: em_pl:**

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27: em_sts:**

28: em_un:**

29: em_vl:**

30: em_htg_hum:**

31: em_htg_inv:**

32: em_htg_other:**

33: em_htg_mus:**

34: em_htg_pln:**

35: em_htg_rod:**

36: em_htg_mam:**

37: em_htg_vrt:**

38: em_sy:**

39: em_htgo_hum:**

40: em_htgo_mus:**

41: em_htgo_other:**

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1335	100.0	1335	6	AX010615	AX010615 Sequence
2	1335	100.0	1335	6	AX010646	AX010646 Sequence
3	1156	86.6	1679	9	BC018747	BC018747 Homo sapi
4	1147.2	85.9	1437	6	AR108865	AR108865 Sequence
5	1146.6	85.9	1630	9	BC024289	BC024289 Homo sapi
6	1145.8	85.8	1659	9	BC014667	BC014667 Homo sapi
7	1136	85.1	1430	6	AX149496	AX149496 Sequence
8	1133.8	84.9	7521	6	AX080951	AX080951 Sequence
9	1129.6	84.6	1353	6	AX277242	AX277242 Sequence
10	1127.6	84.5	1590	9	AK098817	AK098817 Homo sapi
11	1127.2	84.4	1419	12	AF019036	AF019036 Synthetic
12	1124.2	84.1	1401	9	AF027159	AF027159 Homo sapi
13	1123.4	84.1	1642	9	AK093806	AK093806 Homo sapi
14	1121.2	84.0	1673	9	HSIGG1LH	Y14737 Homo sapien
15	1120.2	83.9	1549	6	A21385	A21385 Plasmid DNA
16	1119.8	83.9	1624	9	HSIGG1KH	Y14735 Homo sapien
17	1119.6	83.9	1631	9	AK097010	AK097010 Homo sapi
18	1116.2	83.6	1666	9	BC006402	BC006402 Homo sapi
19	1111.6	83.3	1633	9	AK097367	AK097367 Homo sapi
20	1110.4	83.2	1633	9	AK097859	AK097859 Homo sapi
21	1109.6	83.1	3143	9	BC019046	BC019046 Homo sapi
22	1107	82.9	1637	9	AK093636	AK093636 Homo sapi
23	1104.8	82.8	1404	6	AX268679	AX268679 Sequence
24	1104.4	82.7	1639	9	AK097950	AK097950 Homo sapi
25	1103.2	82.6	1624	9	AK097206	AK097206 Homo sapi
26	1103	82.6	1620	9	AK097366	AK097366 Homo sapi
27	1102.2	82.6	2196	6	AX268709	AX268709 Sequence
28	1102.2	82.6	2226	6	AX268715	AX268715 Sequence
29	1100.4	82.4	1822	9	AK097359	AK097359 Homo sapi
30	1099.6	82.4	1627	9	AK097350	AK097350 Homo sapi
31	1097.8	82.2	1608	9	BC019337	BC019337 Homo sapi
32	1096.6	82.1	2190	6	AX268713	AX268713 Sequence
33	1096.6	82.1	2220	6	AX268719	AX268719 Sequence
34	1095.8	82.1	2193	6	AX268711	AX268711 Sequence
35	1095.8	82.1	2223	6	AX268717	AX268717 Sequence
36	1082.6	81.1	8120	6	AR116673	AR116673 Sequence
37	1082	81.0	4207	6	AX359930	AX359930 Sequence
38	1082	81.0	4207	6	AX382144	AX382144 Sequence
39	1082	81.0	5732	6	AX359932	AX359932 Sequence
40	1082	81.0	5732	6	AX382146	AX382146 Sequence
41	1082	81.0	9183	6	AX359933	AX359933 Sequence
42	1082	81.0	9183	6	AX382147	AX382147 Sequence
43	1072.6	80.3	1465	10	S79307	S79307 Ig gamma -1
44	1071.8	80.3	1605	9	BC025314	BC025314 Homo sapi
45	1071.2	80.2	1602	9	BC014258	BC014258 Homo sapi

ALIGNMENTS

RESULT 1
AX010615
LOCUS AX010615 1335 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 18 from Patent WO9958679.
ACCESSION AX010615
VERSION AX010615.1 GI:9997427
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 18 18-NOV-1999;
Bonnefoy JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON

Pred. No. is the number of results predicted by chance to have a

NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)
Location/Qualifiers
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/db_xref="taxon:32630"
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BASE COUNT 321 a 414 c 360 g 240 t
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Db 1321 TCCTCCGGTAAATGA 1335

RESULT 2
AX010646/c
LOCUS AX010646 1335 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9958679.
ACCESSION AX010646
VERSION AX010646.1 GI:9997455
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 49 18-NOV-1999;
Bonnefoy Jean Yves Marcel Paul (FR); Crowe Scott James (GB); Rapson Nicholas Timothy (GB); Glaxo Group Ltd (GB); Ellis Jonathan Henry (GB); Shearin Jean (US)
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BASE COUNT 240 a 360 c 414 g 321 t

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BASE COUNT 430 a 506 c 452 g 291 t
ORIGIN

Query Match 86.68; Score 1156; DB 9; Length 1679;
Best Local Similarity 92.18; Pred. No. 1.le-226;
Matches 1254; Conservative 0; Mismatches 75; Indels 33; Gaps 2;
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Db 414 GATGCGCAGCAGCTGGTACAGGAGTGGTTCGACCCCTGGGGCCAGGAAACCCCTGGTCAAC 473
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Db 774 GTTAGCCCAAAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCACGACCTGAACCTC 833
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LOCUS AR108865 1437 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6113898.
ACCESSION AR108865
VERSION AR108865.1 GI:12825141
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1437)
AUTHORS Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.
TITLE Human B7.1-specific primatized antibodies and transfectomas
JOURNAL expressing said antibodies
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Location/Qualifiers
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LOCUS Homo sapiens, clone MGC:39273 IMAGE:5440834, mRNA linear PRI 28-FEB-2002
DEFINITION BC024289
ACCESSION BC024289
VERSION BC024289.1 GI:18999464
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1630)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-femail.nih.gov
Tissue procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jeff Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
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to protein.
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64. .1479

FEATURES
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CDS

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott zuiderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Location/Qualifiers

FEATURES

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69. 1508

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ORIGIN

Query Match 85.8%; Score 1145.8; DB 9; Length 1659;
Best Local Similarity 90.6%; Pred. No. 1.3e-224;
Matches 1253; Conservative 0; Mismatches 82; Indels 48; Gaps 1;

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DB 246 CCAGGGAAGGGCTCGAGTGGTTCCTGAAATTTAGATTGAATCTGATAATTATGCAACA 305
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RESULT 7

AX419496
LOCUS AX419496
DEFINITION Sequence 1 from Patent WO0188132.
ACCESSION AX419496
VERSION AX419496.1
KEYWORDS GI:21523919
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

PAT 18-JUN-2002

REFERENCE 1
AUTHORS Hooper,D.C. and Dietzschold,B.
TITLE Rabies virus-specific neutralizing human monoclonal antibodies and
nucleic acids and related methods
JOURNAL Patent: WO 0188132-A 1 22-NOV-2001;
Thomas Jefferson University (US)
FEATURES Location/Qualifiers
source 1..1430
BASE COUNT 326 a 438 c 396 g 270 t
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Best Local Similarity 90.3%; Pred. No. 1.4e-222;
Matches 1249; Conservative 0; Mismatches 80; Indels 45; Gaps 2;
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AX080951
LOCUS AX080951 7521 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 1 from Patent WO0109303.
ACCESSION AX080951
VERSION AX080951.1 GI:13169888
KEYWORDS synthetic construct.
synthetic construct.
artificial sequences.
1 (bases 1 to 7521)
Hermanson,G.G.
Flt-3 ligand-encoding polynucleotide as a polynucleotide-based
vaccine enhancer
Patent: WO 0109303-A 1 08-FEB-2001;
VICAL INCORPORATED (US)
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BASE COUNT 1879 a 1988 c 1858 g 1796 t
ORIGIN

Query Match 84.9%; Score 1133.8; DB 6; Length 7521;
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QY	298	-----GATTTCATAGACTGGGCCAGGGAACA	324
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DB	3150	CTGTCACCGTCTCTCTCAGCTGGGCCCAAGGGCCCATCGGTCTTCCGCCCTGGCACCTCC	3203
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LOCUS	AX277242	1353 bp	DNA linear PAT 06-FEB-2002
DEFINITION	Sequence 27 from Patent WO0175110.		
ACCESSION	AX277242		
VERSION	AX277242.2	GI:18614077	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Hoogenboom, H. R. and Henderikx, M. P.		
TITLE	Mucin-1 specific binding members and methods of use thereof		
JOURNAL	Patent: WO 0175110-A 27 11-OCT-2001;		
COMMENT	Dyax Corporation (US)		
FEATURES	On Feb 7, 2002 this sequence version replaced gi:16548881.		
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ACCESSION AF019036
VERSION AF019036.1 GI:6649879
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pilkington,G.R., Gilmour,J.R. and Gilmour,P.S.
TITLE Three dimensional structure of a fully human IgG1, neutralizing
antibody for RSV
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1419)
AUTHORS Pilkington,G.R., Gilmour,J.R. and Gilmour,P.S.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1997) Intracel Corp., 1871 NW Gilman Blvd,
Issaquah, WA 98027, USA
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DEFINITION Homo sapiens immunoglobulin gamma heavy chain (T6J/g) mRNA, partial
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AF027159.1 GI:2623586
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.
1 (bases 1 to 1401)
Molecular expression of human antibody and prediction of
antigen-binding structure (Abstract)
Proc. Jpn. Soc. Immunol. 24, 639 (1994)
2 (bases 1 to 1401)
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.
Direct Submission
Submitted (29-SEP-1997) Department of Biological Sciences and
Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba
278, Japan
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VERSION
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ORGANISM
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  Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
  NEDO human cDNA sequencing project
  Unpublished
  2 (bases 1 to 1642)
  Isogai, T. and Yamamoto, J.
  Direct Submission
  Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
  Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
  (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
  NEDO human cDNA sequencing project supported by Ministry of
  Economy, Trade and Industry of Japan; cDNA full insert sequencing:
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ACCESSION Y14737
VERSION Y14737.1 GI:2765424
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SOURCE Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1673)
AUTHORS Paterson,T., Innes,J., McMillan,L., Downing,I. and Carter,M.C.
TITLE Variation in IgG1 heavy chain allotype does not contribute to differences in biological activity of two human anti-Rhesus (D) monoclonal antibodies
JOURNAL Immunotechnology 4 (1), 37-47 (1998)
MEDLINE 98326459
PUBMED 9661813
REFERENCE 2 (bases 1 to 1673)
AUTHORS Paterson,T.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1997) T. Paterson, National Science Laboratory, Scottish Nat. Blood Transfusion Service, 12 Bristo Place, Edinburgh, EH1 1EZ, Scotland, UK

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Job time : 2682.46 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run On: April 26, 2003, 04:55:21 ; Search time 1766.31 seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaagtgcagctggtggagtc.....ccctgtctcgggtaaatga 1335

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

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3: em_estin.*
4: em_estnu.*
5: em_estov.*
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9: gb_est1.*
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12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	898.8	67.3	1020	14	BQ062878
2	860.8	64.5	947	14	BQ709771
3	847.2	63.5	958	14	BQ706140
4	839.2	62.9	926	12	BG755166
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6	831.2	62.3	901	13	BM007892

7	826.4	61.9	918	14	BQ708022	BQ708022	AGENCOURT
8	821.2	61.5	1029	14	BQ063185	BQ063185	AGENCOURT
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10	819.6	61.4	995	14	BM914540	BM914540	AGENCOURT
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12	797	59.7	1031	14	BQ064886	BQ064886	AGENCOURT
13	794.2	59.5	936	14	BQ711727	BQ711727	AGENCOURT
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18	780.4	58.5	991	14	BQ708936	BQ708936	AGENCOURT
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21	772.2	57.8	981	14	BM914528	BM914528	AGENCOURT
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24	758.2	56.8	945	14	BQ712403	BQ712403	AGENCOURT
25	756.2	56.6	961	14	BQ710233	BQ710233	AGENCOURT
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32	737.6	55.3	906	14	BQ711709	BQ711709	AGENCOURT
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34	730.4	54.7	919	14	BQ709339	BQ709339	AGENCOURT
35	729.6	54.7	936	14	BQ707530	BQ707530	AGENCOURT
36	728.6	54.6	1014	14	BM914505	BM914505	AGENCOURT
37	727.4	54.5	855	13	BM007689	BM007689	603617119
38	727.2	54.5	973	14	BQ708902	BQ708902	AGENCOURT
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40	726.4	54.4	888	12	BG757604	BG757604	602714780
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42	725.4	54.3	925	14	BQ709853	BQ709853	AGENCOURT
43	725.2	54.3	991	14	BQ707621	BQ707621	AGENCOURT
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ALIGNMENTS

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BQ062878
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BQ062878
BQ062878.1 GI:19890085
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 1020)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2094 row: h column: 21
High quality sequence start: 21
High quality sequence stop: 681.
Location/Qualifiers


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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      239 a      344 c      269 g      166 t      2 others
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Query Match      67.3%; Score 898.8; DB 14; Length 1020;
Best Local Similarity 97.8%; Pred. No. 1.1e-206;
Matches 921; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

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Db      |||||||
QY 453 GACGGTGTCTGTGGAACTCAGCGGCCCTGACGAGCGGCTGCACACCTTCCCGGCTGTCT 512
Db      |||||||
QY 96  GACGGTGTCTGTGGAACTCAAGCGCCCTGACGAGCGGCTGCACACCTTCCCGGCTGTCT 155
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QY 513 ACAGTCTCTAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCCTTCAGCAGCTTGGG 572
Db      |||||||
QY 156 ACAGTCTCTAGGACTCTACTCCCTCAGCAGCGGTGACCGTGCCCTTCACGAGCTTGGG 215
Db      |||||||
QY 573 CACCCAGACCTACATCTGCAAGCTGAATCACAGCCCGACCAACCAAGTGTGACAGAA 632
Db      |||||||
QY 216 CACCCAGACCTACATCTGCAAGCTGAATCACAGCCCGACCAACCAAGTGTGACAGAA 275
Db      |||||||
QY 633 AGTGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCCGTCGCCAGCAGCTGAAC 692
Db      |||||||
QY 276 AGTTGAGCCCAATCTTGTGACAAAACCTACACATGCCACCCGTCGCCAGCAGCTGAAC 335
Db      |||||||
QY 693 CGCGGGGACCGTCACTCTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTC 752
Db      |||||||
QY 336 CCGGGGGGACCGTCACTCTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTC 395
Db      |||||||
QY 753 CCGGACCCCTGAGTCACTATGCGTGTGGTGGAGCGGAGCCAGCAAGACCTCAGGTCAA 812
Db      |||||||
QY 396 CCGGACCCCTGAGTCACTATGCGTGTGGTGGAGCGGAGCCAGCAAGACCTCAGGTCAA 455
Db      |||||||
QY 813 GTTCAACTGTGTAGTGACCGCGGTGGAGGTGCATAATGCCAAGCAAGCGCGGGAGGA 872
Db      |||||||
QY 456 GTTCAACTGTGTAGTGACCGCGGTGGAGGTGCATAATGCCAAGCAAGCGCGGGAGGA 515
Db      |||||||
QY 873 GCAGTACAACGACGCTACCGTGTGTGTCAGCTCTTCCAGCGTCTCGCAGCAGACTGGCT 932
Db      |||||||
QY 516 GCAGTACAACGACGCTACCGTGTGTGTCAGCTCTTCCAGCGTCTCGCAGCAGACTGGCT 575
Db      |||||||
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Db      |||||||
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QY 993 AACCATCTCCAAAGCCAAAGGCGGCCCGGAGAACCAACAGGTGTACACCTGCCGCCATC 1052
Db      |||||||
QY 636 AACCATCTCCAAAGCCAAAGGCGGCCCGGAGAACCAACAGGTGTACACCTGCCGCCATC 695
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QY 1053 CCGGATGAGTGAACCAAGAACAGGTGACCTGACCTGCTCAAGGCTTCTATCC 1112
Db      |||||||
QY 696 CCGGATGAGTGAACCAAGAACAGGTGACCTGACCTGCTGCTCAAGGCTTCTATCC 755
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QY 1113 CAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCGACCGGA--GAACAACATACAAGACC 1170
Db      |||||||
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QY 1171 AGCCCTCCCGTCTGACTCCGACGCGCTCTTCTTCCCTCTACAGCAAGCTCACCGTGCAC 1230
Db 816 ACCTCTCNCGTGTGACTCCGACGCGCTCTTCTTCCCTCTACAGCAAGCTCACCGTGGGA 875
QY 1231 AAGCAGAGTGGCAGCAGGAGGAACTCTTCTCATGCTCCGTGATCATGAGCTCTGCAC 1290
Db 876 CAGAGCAGTGGCAGCAGGGAACGCTCTTCTCATGCTCCGTGATCATGAGCTCTGCAC 935
QY 1291 AACCACTACGCAAGAGCGCTCTCCCTGCTCCCGGTAA 1332
Db 936 AACCACTACGCAAGAGCGCTCTCCCTGCTCTCGGGTAA 977

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DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
5', mRNA sequence.
ACCESSION  BQ709771
VERSION    BQ709771.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 947)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            plate: L10M2466 row: m column: 16
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                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCAGCAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
                225 a      320 c      252 g      150 t

BASE COUNT      225 a      320 c      252 g      150 t
ORIGIN
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Best Local Similarity 99.2%; Pred. No. 1.6e-197;
Matches 865; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 9   GGAAGTCTAGGCGCCCTGACACGCGGTGCACACCTCCCGGCTGTCTCTACAGTCTCAG 68
Db      |||||||
QY 524 GACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCGCTCCAGCAGCTTGGGACCCAGACT 583
Db      |||||||
QY 69  GACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCGCTCCAGCAGCTTGGGACCCAGACT 128
Db      |||||||
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QY	584	ACATCTGCAACGTGAATACAAAGCCAGCAACACCAAGGTGGACAAAGTGGAGCCCA	643
Db	129	ACATCTGCAACGTGAATACAAAGCCAGCAACACCAAGGTGGACAAAGTGGAGCCCA	188
QY	644	AATCTTGTGACAAACTACACATGCCACCGTGGCCAGCAGCTGAACCTCGGGGGCAC	703
Db	189	AATCTTGTGACAAACTACACATGCCACCGTGGCCAGCAGCTGAACCTCGGGGGCAC	248
QY	704	CGTCAGCTTCTCTTCCCGCCCAAAAGCAAGCACCCTCATGATCTCCCGGACCCCTG	763
Db	249	CGTCAGCTTCTCTTCCCGCCCAAAAGCAAGCACCCTCATGATCTCCCGGACCCCTG	308
QY	764	AGTGCACATCGGTGGTGGAGGTGCATAATGCCAAGCAAGCCGGGAGGAGCAGTACA	823
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QY	824	ACGTGGACGGGTGGAGGTGCATAATGCCAAGCAAGCCGGGAGGAGCAGTACAACA	883
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QY	1004	AAGCCAAAGGAGCCCGGAGGAGTGCATACACCTGCCCCATCCCGGGATGAGC	1063
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QY	1184	TGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGACAGTGGC	1243
Db	729	TGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGACAGTGGC	788
QY	1244	AGCAGGGAACGCTTCTTCTCATGCTCGCTGATGAGCTCTGCACAACTACACGC	1303
Db	789	AGCAGGGAACGCTTCTTCTCATGCTCGCTGATGAGCTCTGCACCACTACACGC	848
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Db	849	AGAAGAGCTCTCCCTGTCTCCGGGTAATGA	880
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ACCESSION	5', mRNA sequence.		
VERSION	BQ706140.1 GI:21845039		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 958)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-r@mail.nih.gov		
	Tissue Procurement: Dr. Mark Watson		
	cDNA Library Preparation: Rubin Laboratory		

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM2464 row: a column: 01 High quality sequence stop: 705. Location/Qualifiers 1. 958 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6277512" /lone_lib="NIH_MGC_113" /note="Organ: spleen; Vector: pOTB7; Site:1; XhoI; Site:2; EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."			
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QY	822	GTACGTGACCGGTGGAGGTGCATATGCCAAGCAAGCCCGGGAGGAGCAGTACAA	881
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QY 1182 GCTGACTCCGACGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGACGGTG 1241
DB 731 GCTGACTCCGACGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAGACGGTG 790
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ACCESSION BG755166
VERSION BG755166.1 GI:14065819
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1695 row: 0 column: 21
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Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 225 a 309 c 244 g 148 t
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Query Match 62.9%; Score 839.2; DB 12; Length 926;
Best Local Similarity 97.9%; Pred. No. 2.7e-192;
Matches 850; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 528 CTACTCCTCTCAGACGCTGGTGACCGTGCCTCCAGCAGCTTGGGCCACCCAGACCTACAT 587

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DB 62 CTACTCCTCTCAGACGCTGGTGACCGTGCCTCTCAGCAGCTTGGGCACCCAGACCTACAT 121
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QY 708 AGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT 767
DB 242 AGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT 301
QY 768 CACATCGCTGGTGGTGGAGCTGAGCCACCAAGACCTTGAGGTCAAGTTCACCTGGTACGT 827
DB 302 CACATCGCTGGTGGTGGAGCTGAGCCACCAAGACCTTGAGGTCAAGTTCACCTGGTACGT 361
QY 828 GGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAC 887
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QY 1188 CTCGACGCGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCA 1247
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RESULT 5
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LOCUS AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
DEFINITION 5', mRNA sequence.
ACCESSION BG708857
VERSION BG708857.1 GI:21847756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 988)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

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Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LECM2464 row: c column: 02
High quality sequence stop: 716.
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II kit (Life Technologies). Note: this is a
NIH MGC Library."

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BASE COUNT	230 a	338 c	258 g	162 t	ORIGIN	
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Db	16	ACTGGGCGCAGGGAAACGCTGTG	TCAACCGTCTCTCGGCTCC	CAACAAGGGCCATCGGTCT	75	
QY	368	TCCCCCTTGGCACCCCTCTCC	AAAGAGCACTCTGGGGCAC	AGCGCCCTGGGTGCTGG	427	
Db	76	TCCCCCTTGGCACCCCTCTCC	AGAGCACTCTGGGGCAC	AGCGCCCTGGGTGCTGG	135	
QY	428	TCAAGGACTACTTCCCGGAA	CCGGTGAGGTGTCTGGA	ACTCAGGCGCCCTGACCA	487	
Db	136	TCAAGGACTACTTCCCGGAA	CCGGTGAGGTGTCTGGA	ACTCAGGCGCCCTGACCA	195	
QY	488	GCGTGCACACCTTCCCGGCT	CTCTACAGTCTCAGAC	TCTACTCCTCAGCAGCTGG	547	
Db	196	GCGTGCACACCTTCCCGGCT	CTCTACAGTCTCAGAC	TCTACTCCTCAGCAGCTGG	255	
QY	548	TGACCGTGCCCTCCAGCAG	CTTGGGCACCCAGACCT	TACATCTGCAAGTGAAT	607	
Db	256	TGACCGTGCCCTCCAGCAG	CTTGGGCACCCAGACCT	TACATCTGCAAGTGAAT	315	
QY	608	CCAGCAACACAAGGTGG	ACAAGAACTGGAGGCC	CCCAATCTTGTGACAAA	667	
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QY	668	GCCACCGTGCCCGAGC	ACCTGAATCTCGGGGGG	CACCGTACGTCTCTTCC	727	
Db	376	GCCACCGTGCCCGAGC	ACCTGAATCTCGGGGGG	CACCGTACGTCTCTTCC	435	
QY	728	AACCCAAAGGACACCC	TATGATCTCCCGGAC	CCCTGAGGTACATGCG	787	
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QY	788	TGAGCCACGAAGACCC	TGAGTCAAGTTC	AACTGGTACGTGGAG	847	
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QY	848	ATGCCAAGACAAAGCC	CGGGAGGAGCAGT	TACACACGTCACCGT	907	
Db	556	ATGCCAAGACAAAGCC	CGGGAGGAGCAGT	TACACACGTCACCGT	615	
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DB	676	AAGCCCTCCAGCCCCCATCTCAGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAA	735
QY	1028	CACAGGTGTACACCTTGCCTCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCTGA	1087
DB	736	CACAGGTGTACACCTTGCCTCCCATCCCGGGATGAGCTGACCAAGAACCAGGTACGCTGA	794
QY	1088	CCTGCCTGGTCAAGGGCTTCTATCCACCGACATCGCGGTGGAGTGGAGAGACAATGGGC	1147
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QY	1148	AG-CCGGAGAACAACTACAAGACACCGCTCCCGTG---CTGGACTCGGACGGC-TCCTT	1202
DB	855	AGCCCGGAGAACAACTACCAGACACCGCTCCCGTGCTGGAATCCGAGGCTTCCTT	914
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LOCUS	603617577F1	NIH_MGC_113	Homo sapiens cDNA clone IMAGE:5450611 5',
DEFINITION	BM007892	901 bp	mRNA linear EST 30-OCT-2001
ACCESSION	BM007892		mRNA sequence.
VERSION	BM007892.1	GI:16522233	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 901)		
JOURNAL	NTH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LRCMI939 row: j column: 20 High quality sequence stop: 834. Location/Qualifiers 1..901 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5450611" /clone_lib="NIH_MGC_113" /lab_host="DH10B (phage-resistant)" /notes="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 209 a 315 c 234 g 143 t		
FEATURES	source		
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Best Local Similarity	97.7%	pred. No.	2.3e-190;
Matches	864; Conservative	0; Mismatches	18; Indels
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BASE COUNT	209 a	315 c	234 g	143 t
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Query Match	62.3%; Score 831.2; DB 13; Length 901;			
Best Local Similarity	97.7%; Pred. No. 2.3e-190;			
Matches 864; Conservative	0; Mismatches 18; Indels 2; Gaps 2;			

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QY 372 CTTGGGCAACCTCTCTCCAAAGACACCTCTCTGGGGGACAGCGGCCCTGGGTGCTGTCTAA 431
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QY 432 GGACTACTTCCCGAAGCCGCTGACGGTGTCTGTAACCTCAGGCGCCCTGACCAAGCGCGT 491
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QY 612 CAACCAAGGTGGACAAAGAGTGGAGCCCAATCTTGTGACAAACTCACACATGCC 671
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DEFINITION AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
5', mRNA sequence.
ACCESSION BQ708022
VERSION BQ708022.1 GI:21846921
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2469 row: 1 column: 20
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FEATURES

source

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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Db 68 CCCCTGTGCACCTCTCTCCAGAGCACCTCTGGGGGACAGCGCCCTGGGTGCTGCTGT 127

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ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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					Contact: Robert Strausberg, Ph.D.	Email: rcapbs@mail.nih.gov	Tissue Procurement: Dr. Mark Watson	cDNA Library Preparation: Rubin Laboratory	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
					DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov	Plate: L1CM2474	row: m column: 20
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						/lab_host="DH10B (phage-resistant)"	/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
					BASE COUNT	218 a	295 c	230 g	143 t
					ORIGIN				1 others
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QY	505	GCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCGTCCAGC	564						
Db	61	GCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCGTCCAGC	120						
QY	565	AGCTTGGGACCCAGACCTACATCTGCAAGTGTAATCACAGCCCGACACACCAAGGTG	624						
Db	121	AGCTTGGGACCCAGACCTACATCTGCAAGTGTAATCACAGCCCGACACACCAAGGTG	180						
QY	625	GACAAGAAGTGGAGGCCAATCTTGTGACAAACTCACACATGCCACCGTGCCACGCA	684						
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QY	685	CCTGAACTCGGGGGGACCGTCAAGTCTTCTCTCCCGCCCAAAACCAAGGACACCGTC	744						
Db	241	CCTGAACTCGGGGGGACCGTCAAGTCTTCTCTCCCGCCCAAAACCAAGGACACCGTC	300						
QY	745	ATGATCTCCGGACCCCTGAGGTACATGCGTGTGTGGACGTGAGCCAGAACCCCT	804						
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QY	805	GAGGTCAAGTTCACCTGTCAGTGGACGGCTGAGGTGCATATGCCACAGCAAAAGCCG	864						
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QY	865	CGGAGGAGCAGTACACAGCAGCTACCGGTGTGGTGTGAGCGTCTCTACCGCTCTGCACAG	924						

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Db	16	GATTGGGGCCAGGGAACGCTGTCACCGTCTCTCTCAGCCTCCACCAAGGCGCCATCGGTC	75		
QY	367	TTCCCCCTGGCACCTCTCTCAAGAGACACTCTGGGGGACAGGGCCCTGGGCTGCCG 426			
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QY	487	GGCGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTG 546			
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QY	547	GTGACCGTGCCCTCAGCAGACTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAG 606			
Db	256	GTGACCGTGCCCTCAGCAGACTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAG 315			
QY	607	CCGAGCAACAAAGTGGACAAGAAAGTGGAGCCCAAACTTTGTGACAAACTCACACA 666			
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QY	667	TGCCCCACCGTCCCGCAGCACCTGAATCTCGGGGGCACCCTCAGTCTTCTCTTCCGCCCA 726			
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QY	727	AAACCCAAAGGACACCTCATGATCTCCGGGACCCCTGAGGTTCATCGGTGGTGGTGGAC 786			
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QY	967	AAAGCCCTCCGAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGACGCCCCGAGAA 1026			
Db	676	AAAGCCCTCCGAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGACGCCCCGAGAA 735			
QY	1027	CCACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGTACCAAGAACCAAGGTTCAGCCTG 1086			
Db	736	CCACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGTACCAAGAACCAAGGTTCAGCCTG 795			
QY	1087	ACCTGCGTGGTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGG -AGAGCAATGG 1145			
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DEFINITION	AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096				
	linear EST 16-JUL-2002				

5', mRNA sequence.	
ACCESSION	BQ711291
VERSION	BQ711291.1
KEYWORDS	GI:21850190
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 881)
COMMENT	NIH-MGC http://www.ncbi.nlm.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2468 row: c column: 01 High quality sequence stop: 721.
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BASE COUNT	220 a 285 c 237 g 139 t
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Query Match	60.3%; Score 805.6; DB 14; Length 881;
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QY	576 CCAGACCTACATCTGCAACGTTGAATCACAGCCAGCAGCAACACCAAGGTGGACAGAAAGT 635
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	181 GGGGGCACCCTGACGTCTTCCTTTCCCGCCAAAACCCNAGACACCCCTCATGATCTCCCG 240
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QY	816 CAACTGGTACGTGGACGCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCA 875
Db	
	301 CAACTGGTACGTGGACGCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCA 360
QY	876 GTACAACAGCAGCTACCGTGTGGTACCGTCTCTACCGTCTCTGCACAGGACTGGCTGAA 935
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QY 1116 CGACATCCCTGGTGGGAGAGCAATGGCGAGCCGAGAACAACTACAGACCAAGCC 1175
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DEFINITION AGENCOURT_6887080 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929343
5', mRNA sequence.
ACCESSION BQ064886
VERSION BQ064886.1 GI:19893932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2107 row: e. column: 24
High quality sequence stop: 573.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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BASE COUNT 248 a 349 c 271 g 162 t 1 others
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Best Local Similarity 94.2%; Pred. No. 4.5e-182;
Matches 838; Conservative 0; Mismatches 51; Indels 1; Gaps 1;
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QY 455 CGTGTCGTGGAACTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCCGGCTGTCTAC 514
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QY 515 AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTCCAGCAGCTTGGGCA 574
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LOCUS BQ711727 936 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8495330 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301961
5', mRNA sequence.
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VERSION BQ711727.1 GI:21850626
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2518 row: k column: 18
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                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
BASE COUNT 231 a 306 c 245 g 152 t 2 others
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Query Match 59.5%; Score 794.2; DB 14; Length 936;
Best Local Similarity 98.1%; Pred. No. 2.1e-181;
Matches 824; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
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VERSION BQ705928.1 GI:21844827
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2382 row: k column: 20
High quality sequence stop: 619.
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            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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BASE COUNT 235 a 318 c 240 g 147 t
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QY 581	CTTACATCTGCAACGTGAATCAAGCCCGAGCAACACAAAGGTGGACAGAAAGTGGAGC	640		
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DB 241	CTGAGTGCACATCGTGGTGGTGACGTGAGCCAGAGACCTTGAGGTCAAGTTCAACT	300		
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QY 1001	CNAAGCCAAAGGGCAGCCCGAGAACACAGTGTACACCTTGCCCGCCATCCCGGATG	1060		
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QY 1241	GGCAGCAGGGGAACGCTTCTCATGCTCCGTTGATGATGAGGCTCTGCACAAACCTACA	1300		
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REFERENCE	1	(bases 1 to 980)
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Note: LNCM2002 row: k column: 02 High quality sequence stop: 689.	
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	/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming, Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."	
BASE COUNT	235 a 332 c 256 g 155 t	2 others
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Query Match	59.08;	Score 788; DB 14; Length 980;
Best Local Similarity	97.1%;	Pred. No. 6.7e-180;
Matches	824; Conservative	0; Mismatches 21; Indels 4; Gaps 2;
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Db	1	
Qy	395	CCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTTCAGGACTACTTCCCGAACCGGTGA 454
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Qy	455	CGGTGTCGTGGAACCTAGGCGCCCTGACACAGCGCGGTGCACACCTTCCCGGCTGTCTCTAC 514
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Qy	515	AGTCCTCAGGACTCTACTCCTCAGACGCTGGTGTGACCGTGCCTCCAGCAGCTTGGGCA 574
Db	181	
Qy	575	CCAGACCTACATCTGCAACGCTGAATCACAAGCCACGACACCAAGGTGCACAAGAAAG 634
Db	241	CCAGACCTACATCTGCAACGCTGAATCACAAGCCACGACACCAAGGTGCACAAGAAAG 300
Qy	635	TGGAGCCCAANTCTGTGACAAAACCTCACACATGCCACACCGTGCCAGCACCTGAACTCG 694
Db	301	TTGAGCCCAANTCTGTGACAAAACCTCACACATGCCACACCGTGCCAGCACCTGAACTCC 360
Qy	695	CGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCC 754
Db	361	TGGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCC 420
Qy	755	GGACCCCTG-AGGTTCACATCGCTGGTGGTGTGAGCGTGAGCCACCAAGACCTTGAGGTCAAG 813
Db	421	GGACCCCTGAGGTTCACATCGCTGGTGGTGTGAGCGTGAGCCACCAAGACCTTGAGGTCAAG 480
Qy	814	TTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGAGGAG 873
Db	481	TTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGAGGAG 540

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 268.58 Seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgggtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*
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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	1335	21	AAZ34748 Humanised anti-CD2
2	1149.2	86.1	1442	22	AAZ34748 Plasmid Glambda-1A
3	1147.8	86.0	1798	21	AAC98220 Human colon cancer
4	1147.2	85.9	1437	19	AAV35487 Macaque primatized
5	1147.2	85.9	1437	24	AAAS17245 DNA sequence of a
6	1145.6	85.8	1437	18	AAT13847 Primatized anti-hu
7	1145	85.8	1616	24	AA562785 cDNA sequence #572
8	1143.6	85.7	1576	14	AAQ49944 Human anti-HBs hea
9	1142.8	85.6	1386	14	AAQ49834 Anti-HIV-1 recomb

10	1142.8	85.6	6291	22	AAZ34748	Plasmid Glambda-1A
11	1142.2	85.6	19035	19	AAV61794	Traget plasmid Man
12	1141.8	85.5	1427	19	AAV41431	Plasmid Hu19DHCpcd
13	1141.8	85.5	1427	19	AAV41431	Plasmid Hu19DHCpcd
14	1140.2	85.4	1427	19	AAV41429	Plasmid Hu19BHCpcd
15	1136.6	85.1	1617	24	AA562784	cDNA sequence #571
16	1136	85.1	1430	24	AAK98701	cDNA of the heavy
17	1135	85.0	1347	21	AAZ60599	cDNA encoding a ra
18	1133.8	84.9	7521	22	AAF30315	Bicistronic chimera
19	1131	84.7	1356	22	AAZ20745	Human recombinant
20	1128.8	84.6	6284	19	AAV41427	Plasmid Hu19AHpcd
21	1125.8	84.3	1641	15	AAQ54655	chir84.12 H3 heavy
22	1121.4	84.0	9182	24	ABK10574	Baculovirus expres
23	1121.2	84.0	1644	22	AAZ22593	Human cDNA encodin
24	1119.8	83.9	9182	24	ABL55051	Plasmid pTRABac/9F
25	1118.6	83.8	1549	13	AAQ20066	Encodes heavy chai
26	1117	83.7	1412	13	AAK34965	Sequence of the ch
27	1105.2	82.8	1598	24	ABA02666	Human cDNA encodin
28	1104.8	82.8	1404	22	ABA02666	Humanised HMFGL he
29	1102.2	82.6	2196	22	ABA02690	Humanised HMFGL h
30	1102.2	82.6	2226	22	ABA02696	Humanised HMFGL h
31	1100	82.4	1590	24	ABK34976	Human cDNA encodin
32	1096.6	82.1	2190	22	ABA02694	Humanised HMFGL h
33	1096.6	82.1	2220	22	ABA02700	Humanised HMFGL h
34	1095.8	82.1	2193	22	ABA02692	Humanised HMFGL h
35	1095.8	82.1	2223	22	ABA02698	Humanised HMFGL h
36	1089	81.6	2974	22	AAH98397	Synthetic EST-deri
37	1082.6	81.1	8119	20	AAH90575	Plasmid pG4V11N35
38	1082.6	81.1	8119	21	AAZ87975	Nucleotide sequenc
39	1082.6	81.1	8120	21	AAZ87975	Humanised anti-IL-
40	1082	81.0	4207	24	AAZ28367	Cytomegalovirus (C
41	1082	81.0	4207	24	AAZ28367	Cytomegalovirus (C
42	1082	81.0	5732	24	AAZ28369	Mouse mammary tumo
43	1082	81.0	5732	24	AAZ28369	Mouse mammary tumo
44	1082	81.0	9183	24	AAZ28370	Alpha-lactalbumin
45	1082	81.0	9183	24	AAZ28309	Alpha-lactalbumin

ALIGNMENTS

RESULT 1
AAZ34748
ID AAZ34748 standard; cDNA; 1335 BP.

XX AAZ34748;

XX 15-FEB-2000 (first entry)

XX Humanised anti-CD23 Mab C11 heavy chain cDNA.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
XX monoclonal antibody; chimeric antibody; humanised antibody;
XX complementarity determining region; CDR; autoimmune disease;
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX graft-versus-host disease; COPD; bronchitis; diabetes;
XX B-cell malignancy; therapy; ds.

XX Homo sapiens.
XX Synthetic.

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.

(GLAX) GLAXO GROUP LTD.
Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
WPI; 2000-053101/04.
P-PSDB; AAY32263.
Cell receptor specific antibodies useful for treating e.g. arthritis,
diabetes, multiple sclerosis and psoriasis -
Claim 17: Fig 4: 81pp; English.
This DNA sequence encodes the heavy chain of humanised anti-CD23
(IgE receptor, FCER1) monoclonal antibody C11, composed of a human
framework (H5IGKV11) and the heavy chain complementarity determining
regions (see AAY32256-58) of murine antibody C11. The invention
provides altered antibodies, such as chimeric or humanised
antibodies, which comprise sufficient of the amino acid sequences
of the C11 light and heavy chain complementarity determining regions
to render them capable of binding to the CD23 type II molecule
expressed on haematopoietic cells. The antibodies are used to block
soluble CD23 formation in human therapy, for the treatment of
arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria,
nephrotic syndrome, glomerulonephritis, inflammatory bowel disease,
ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies,
allergic asthma, intrinsic asthma, acute asthmatic exacerbation,
rhinitis, eczema, graft-versus-host disease, COPD, insulinitis,
bronchitis (particularly chronic bronchitis) or diabetes
(particularly type 1 diabetes), and B-cell malignancies (claimed).
They are also useful for studying interactions between CD23 and
various ligands and determining the binding agents.
Sequence 1335 BP; 321 A; 414 C; 360 G; 240 T; 0 other;

Query Match 100.0%; Score 1335; DB 21; Length 1335;
Best Local Similarity 100.0%; Pred. No. 3.1e-251; Indels 0; Gaps 0;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
Qy 61 TCCTGTGAGCTAGCGGATTCACATTTTCAGTGGCTACTGGATGCTGGTCCGGCCAGGCT 120
Db 61 TCCTGTGAGCTAGCGGATTCACATTTTCAGTGGCTACTGGATGCTGGTCCGGCCAGGCT 120
Qy 121 CCAGGAAGGGGCTCGAGTGGTGGTCTGCTGAAATTTAGATTGAAATCTGATAATTATGCAACA 180
Db 121 CCAGGAAGGGGCTCGAGTGGTGGTCTGCTGAAATTTAGATTGAAATCTGATAATTATGCAACA 180
Qy 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Qy 241 CTGTATCTGCAATTAACAGCCTTGAACCCGAGCAGACCCGCTGTTACTGTACAGAT 300
Db 241 CTGTATCTGCAATTAACAGCCTTGAACCCGAGCAGACCCGCTGTTACTGTACAGAT 300
Qy 301 TTCATAGACTGGGCGCAGGAACTAGTCACTCCCTCCTCAGCCTCCACCAAGGGGCCCA 360
Db 301 TTCATAGACTGGGCGCAGGAACTAGTCACTCCCTCCTCAGCCTCCACCAAGGGGCCCA 360
Qy 361 TCGGTCTTCCCTCGGCAACCTCTCCCAAGAGCACCCTCTGGGGGCACAGGGCCCTGGGC 420
Db 361 TCGGTCTTCCCTCGGCAACCTCTCCCAAGAGCACCCTCTGGGGGCACAGGGCCCTGGGC 420
Qy 421 TGCCTGGTCAAGGACTACTTCCCGGAAACCGGTGACGGTGTCTGGAATCTAGGCGCCCTG 480
Db 421 TGCCTGGTCAAGGACTACTTCCCGGAAACCGGTGACGGTGTCTGGAATCTAGGCGCCCTG 480
Qy 481 ACCAGCGGCGTGCACACCTTCCCGGCTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540
Db 481 ACCAGCGGCGTGCACACCTTCCCGGCTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540

Db 481 ACCAGCGGCGTGCACACCTTCCCGGCTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540
Qy 541 AGCGTGGTGACCGTGCCCTTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAAT 600
Db 541 AGCGTGGTGACCGTGCCCTTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAAGGTGAAT 600
Qy 601 CACAAGCCCGAGCAACACCAAGGTGGACAAGATGGAGGCCCAAAATCTTGTGACAAAATCT 660
Db 601 CACAAGCCCGAGCAACACCAAGGTGGACAAGATGGAGGCCCAAAATCTTGTGACAAAATCT 660
Qy 661 CACACATGCCCGACCGTGGCCAGCAGCTGAATCGCGGGGGACCGCTCAGTCTTCTCTTC 720
Db 661 CACACATGCCCGACCGTGGCCAGCAGCTGAATCGCGGGGGACCGCTCAGTCTTCTCTTC 720
Qy 721 CCCCCAAAACCCCAAGACACCCCTCATGATCTCCCGGAGCCCTGAGGTACATCGCTGGTG 780
Db 721 CCCCCAAAACCCCAAGACACCCCTCATGATCTCCCGGAGCCCTGAGGTACATCGCTGGTG 780
Qy 781 GTGGAGCTGAGCCAGACAGACCCCTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAG 840
Db 781 GTGGAGCTGAGCCAGACAGACCCCTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAG 840
Qy 841 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGTC 900
Db 841 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGTC 900
Qy 901 AGCGTCTCTCACCGTCTGACACGAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTC 960
Db 901 AGCGTCTCTCACCGTCTGACACGAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTC 960
Qy 961 TCCAAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCCAAGGGCAGGCC 1020
Db 961 TCCAAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCCAAGGGCAGGCC 1020
Qy 1021 CGAAGAACACAGGTGTACACCTGCGCCCATCCCGGGATGAGTGCACCAAGAACAGGTC 1080
Db 1021 CGAAGAACACAGGTGTACACCTGCGCCCATCCCGGGATGAGTGCACCAAGAACAGGTC 1080
Qy 1081 AGCGTACCTGCTGTGTCAAGGCTTCTATCCAGGAGCATCGCGTGGAGTGGAGGAGC 1140
Db 1081 AGCGTACCTGCTGTGTCAAGGCTTCTATCCAGGAGCATCGCGTGGAGTGGAGGAGC 1140
Qy 1141 AATGGCAGCGGAGAAACAATACAAGACACCGCTCCCGTGTCTGGACTCCCGACGGCTCC 1200
Db 1141 AATGGCAGCGGAGAAACAATACAAGACACCGCTCCCGTGTCTGGACTCCCGACGGCTCC 1200
Qy 1201 TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGAGAGGTGGCAGGAGGGAACGTCTTC 1260
Db 1201 TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGAGAGGTGGCAGGAGGGAACGTCTTC 1260
Qy 1261 TCATGCTCGGTGATGATGAGGCTCTGCACACCACTACACCGCAGAACGCTCTCCCTG 1320
Db 1261 TCATGCTCGGTGATGATGAGGCTCTGCACACCACTACACCGCAGAACGCTCTCCCTG 1320
Qy 1321 TCTCCGGGTAATGA 1335
Db 1321 TCTCCGGGTAATGA 1335
RESULT 2
AAC84208
ID AAC84208 standard; DNA; 1442 BP.
XX
AC AAC84208;
XX
DT 19-MAR-2001 (first entry)
XX
Plasmid Glambda-1Bpcd DNA sequence.
XX
DE Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW Glambda-1; human; virucide; RSV propagation; ds.
XX
OS Homo sapiens.

Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerrary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antinefctive; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.	Homo sapiens.	WO2000053531-A1.	21-SEP-2000.	08-MAR-2000; 2000WO-US05883.	12-MAR-1999; 99US-0124270.	(HUMA-) HUMAN GENOME SCI INC.	Rosen CA, Ruben SM;	WPI; 2000-587534/55.	P-PSDB; AAB53463.	Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer	Claim 1; Page 652; 2104pp; English.	AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and vulnerrary, nephrotropic, antinefctive and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention.	Sequence 1798 BP; 477 A; 529 C; 458 G; 311 T; 23 other;	Query Match 86.0%; Score 1147.8; DB 21; Length 1798; Best Local Similarity 91.0%; Pred. No. 9.9e-215; Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps	QY 2 AGTGTCAGCTGGTGAGGCTGGGGAGCGCTTGCTAAAGCCGGGGGCTCCCTAGACTCT 61	Db 206 AGTGCAGCTGGTGAGGCTGGGGAGCGCTGGTCAGCTGGGAGGCTCCCTAGACTCT 265	QY 62 CCGTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCGGTGGCCACGGCTC 121	Db 266 CCGTGTGCAGCTCTGGATTACCTTTCAGTGGCTATGGCATGGCTGGGTGGCCACGGCTC 325	QY 122 CAGGGNAGGGCTCGATGGGTTCCTCAAAATTAGATTGAATCTCATTAATTATGCAACAC 181	Db 326 CAGGCAAGGGCTGGAGTGGGTGGCATTTATATATATATATATATATATATATATATAT 379	QY 182 ATTATTCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241	Db 380 ACTATGCAGACTCGGTGAAGGCCGATTACCATCTCCAGAGACAATCCRAGACACGC 439	QY 242 TGTATCTGCAATGACAGCTGAAAACCGAGGACACACGCCGTGTTACTGTACAGATT 301	Db 440 TGTATCTGCAATGACAGCTGAGAGCTGAGGACACGCTGCTATATCTGCTGCGARAG 499
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QY	1096	GTCAAAGGCTTCTATCCCAAGCAGACATCGCCGTGGAGTGGGAGAGCAATGGCGACGCCGAG	1155
Db	1198	GTCAAAGGCTTCTATCCCAAGCAGACATCGCCGTGGAGTGGGAGAGCAATGGCGACGCCGAG	1257
QY	1156	AACAACCTACAAGACACAGCCTCCCGTGTGGACTCCGACGCGCTCCTTCTTCTCTACAGC	1215
Db	1258	AACAACCTACAAGACACAGCCTCCCGTGTGGACTCCGACGCGCTCCTTCTTCTCTACAGC	1317
QY	1216	AACTCACCCTGGACAAAGACAGGCTGGCAGCAGGGAACGCTCTTCTCATGTCGCGTGATG	1275
Db	1318	AACTCACCCTGGACAAAGACAGGCTGGCAGCAGGGAACGCTCTTCTCATGTCGCGTGATG	1377
QY	1276	CATGAGGCTCTGCACAAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAATGA	1335
Db	1378	CATGAGGCTCTGCACAAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAATGA	1437
RESULT	5		
AAAS17245			
ID	AAAS17245	standard; DNA; 1437 BP.	
XX			
AC	AAAS17245;		
XX			
DT	12-MAR-2002	(first entry)	
XX			
DE		DNA sequence of a primatised form of the heavy chain of 7B6 antibody.	
XX			
KW		Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;	
KW		neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;	
KW		B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;	
KW		tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;	
KW		graft-vs-host disease; immunosuppression; organ rejection;	
XX		interleukin-2; IL-2; mutant; ds.	
XX			
OS		Chimeric - Homo sapiens.	
OS		Chimeric - Macaca sp.	
OS		Synthetic.	
XX			
Key		Location/Qualifiers	
FF		1..1437	
FT		/*tag= a	
FT		/product= "Heavy chain of 7B6 antibody"	
XX			
PN		WO200189567-A1.	
XX			
PD		29-NOV-2001.	
XX			
PF		22-MAY-2001; 2001WO-US16364.	
XX			
PR		22-MAY-2000; 2000US-0576424.	
XX			
PA		{ IDEC- } IDEC PHARM CORP.	
XX			
PI		Anderson DR, Hanna N, Brams P;	
XX			
WP		WPI; 2002-089895/12.	
DR		P-PSDB; AAU11644.	
XX			
PT		Use of monoclonal antibody which specifically binds to B7.1 antigen	
PT		CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,	
PT		treating cancer, graft-vs-host disease and autoimmune disease such as	
XX		allergy	
XX			
PS		Example 8; Fig 4b; 89pp; English.	
XX			
CC		The present invention relates to a new use of a monoclonal antibody	
CC		which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen	
CC		(CD86) for inducing the apoptosis of B7+ cells. The invention is	
CC		useful for treating diseases such as B cell cancer, lymphoma, a	
CC		cancer where B cells promote the growth and/or metastasis of tumours,	
CC		B cell lymphoma; B cell leukaemia, and autoimmune diseases such as	
CC		idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,	

CC	type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC	anemia, inflammatory bile disease, allergy, multiple sclerosis
CC	or graft-vs-host disease. The antibody is useful for immunosuppression
CC	in a human or animal and for treating or preventing resistance to or
CC	rejection of transplanted organ or tissue for treating proliferative
CC	and hyperproliferative diseases, for treating reversible obstructive
CC	airways disease, intestinal inflammations and allergies e.g. Crohn's
CC	disease and ulcerative colitis, food-related allergies e.g. migraine,
CC	rhinitis and eczema, and other types of allergies. The present nucleic
CC	acid sequence encodes the heavy chain of 7B6, a primatised antibody
CC	used in the invention to induce apoptosis.
XX	
SQ	Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;
Query Match 85.9%; Score 1147.2; DB 24; Length 1437;	
Best Local Similarity 90.7%; Pred. No. 1.3e-214;	
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps	
QY	1 GAGGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAGCCGGGGGTCCTTAGACATC 60
DB	
DB	58 GAGGTGCACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCTGGCGGTCCCTGAGATC 117
QY	61 TCCTGTGCAGCTACGGCAATTCATTTTCAGTGGCTACTGGATGCTCTCGCCAGGCT 120
DB	
DB	118 TCCTGTGCAGTCTCTGGATTCACCTTCAGTGACCACCTACATGATTATGGTTCGCCAGGCT 177
QY	121 CCAGGGAAGGGCTCCAGTGGGTGCTGGAATTAGATTTGAATCTGATATATGCAACA 180
DB	
DB	178 CCAGGGAAGGGCGGAGTGGGTAGGTTTCATTAGAAACAACCGAACCCTGGGACAACA 237
QY	181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB	
DB	238 GAATPACCCCGCTGTGTGAAGACAGATTACCACATCTCCAGAGATGATTCCAAAAGCATC 297
QY	241 CTGTATCTGCAATGAACAGCCTGGAACCGGAGGACACAGCGGTGATTACTGTAC --- 296
DB	
DB	298 GCCTATCTGCAATGAGCAGCCTGAAATTCGGAGACACGGCGCTCTATTACTGTACTACA 357
QY	297 -----AGATTTCATAGACTGGGCG 315
DB	
DB	358 TCCTACATTTACATTCGCGGGTGGTGTCTGTATGGAGGTTACTTCGAATTCCTGGGCG 417
QY	316 CAGGGAACACTAGTCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG 375
DB	
DB	418 CAGGGCGCCCTGGTGCACCGTCTCTCAGCTAGCACCAAGGGGCCATCGGTCTTCCCCCTG 477
QY	376 GCACCTTCCTCCAAGAGCACCCTCTGGGGGCACAGCGGCCCTCGGGTGCCTGTGTCAGAGAC 435
DB	
DB	478 GCACCTTCCTCCAAGAGCACCCTCTGGGGGCACAGCGCCCTGGGTGCTCCTGTGTCAGAGAC 537
QY	436 TACTTCCCGGAACCGGTGACGGTGTCTGTGGAATCTAGGGGCCCTTGACAGCGCGGTGTCAC 495
DB	
DB	538 TACTTCCCGGAACCGGTGACGGTGTCTGTGGAATCTAGGGGCCCTTGACAGCGCGGTGTCAC 597
QY	496 ACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTCTCCTCAGCAGCGGTGTGACCCGTG 555
DB	
DB	598 ACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTCTCCTCTCAGCAGCGGTGTGACCCGTG 657
QY	556 CCCTCCAGCAGCTTGGCACCACCCAGACCTACATCTGCAACGTGAATCACAGCCCAAGCAAC 615
DB	
DB	658 CCCTCCAGCAGCTTGGCACCACCCAGACCTACATCTGCAACGTGAATCACAGCCCAAGCAAC 717
QY	616 ACCAAGTGGACAAAGAATGGAGGCCAAATCTTTGTGACAAAACCTCACACATGCCCAACCG 675
DB	
DB	718 ACCAAGTGGACAAAGAAGCAGAGGCCAAATCTTTGTGACAAAACCTCACACATGCCCAACCG 777
QY	676 TGCCACGACCTGAACCTCGCGGGGGCACCGTCAAGTCTTCTCTTCCCGCCCAAAACCCCAAG 735
DB	
DB	778 TGCCACGACCTGAACCTCTCGGGGGACCGTCAAGTCTTCTCTTCCCGCCCAAAACCCCAAG 837
QY	736 GACACCTCATGATCTCCCGGACCCCTCAGGTGCACATGCGTGGTGACGTGAGCCAC 795
DB	
DB	838 GACACCTCATGATCTCCCGGACCCCTCAGGTGCACATGCGTGGTGACGTGAGCCAC 897


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Db 778 TGCCACCACCTGAACCTCTGGGGGACCCTGCTACTCTCTTCCCTCCCAAAACCCAAAG 837
QY 736 GACACCTCATGATCTCTCCCGACCCCTGAGGTACATGCGTGGTGTGAGCGTGAGCCAC 795
PT |||||||
Db 838 GACACCTCATGATCTCTCCCGACCCCTGAGGTACATGCGTGGTGTGAGCGTGAGCCAC 897
QY 796 GAGACCTCTGAGTCAAGTTCACTGGTACGTGGGCGGTGAGGTGCATATATGCCAAG 855
PT |||||||
Db 898 GAGACCTCTGAGTCAAGTTCACTGGTACGTGGGCGGTGAGGTGCATATATGCCAAG 957
QY 856 ACAAGCCGGGAGGAGCAGTACACAGCAGTACCGTGTGTGTCAGCTCTCACCGTC 915
PT |||||||
Db 958 ACAAGCCGGGAGGAGCAGTACACAGCAGTACCGTGTGTGTCAGCTCTCACCGTC 1017
QY 916 CTGACACGAGACTGGCTGAATGCAAGGAGTACAAAGTCAAGTCTCCCAACAAAGCCCTC 975
PT |||||||
Db 1018 CTGACACGAGACTGGCTGAATGCAAGGAGTACAAAGTCTCCCAACAAAGCCCTC 1077
QY 976 CCAGCCCCCATCGAGAAACCATCTCAAGCCAAAGGGCAGCCCGAGAACACACAGGTG 1035
PT |||||||
Db 1078 CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTG 1137
QY 1036 TACACCTCTGCCCCATCCCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCCCTG 1095
PT |||||||
Db 1138 TACACCTCTGCCCCATCCCGGGATGAGCTGACCAAGAACAGCTCAGCTGACCTGCCCTG 1197
QY 1096 GTCAAGGCTTCTATCCAGCAGACATCGCGGTGGTGGAGTGGGAGAGCAATGGGAGCGCGAG 1155
Db 1198 GTCAAGGCTTCTATCCAGCAGACATCGCGGTGGTGGAGTGGGAGAGCAATGGGAGCGCGAG 1257
QY 1156 AACCACTACAGACACCGCTCCCGTGGTGGACTCCGAGGGCTCTTCTCTCTACACG 1215
Db 1258 AACCACTACAGACACCGCTCCCGTGGTGGACTCCGAGGGCTCTTCTCTCTACACG 1317
QY 1216 AAGCTCACCTGGACAAAGAGCAGTGGCAGCGAGGGAAGCTTCTCATGCTCCGTTGATG 1275
Db 1318 AAGCTCACCTGGACAAAGAGCAGTGGCAGCGAGGGAAGCTTCTCATGCTCCGTTGATG 1377
QY 1276 CATGAGGCTCTGCACACCACTACACGACAGAGAGCCTCTCCCGTGTCTCCGGTAAATGA 1335
Db 1378 CATGAGGCTCTGCACACCACTACACGACAGAGAGCCTCTCCCGTGTCTCCGGTAAATGA 1437

RESULT 7
AAS62785
ID AAS62785 standard; cDNA; 1616 BP.
AC AAS62785;
AT
DT 14-FEB-2002 (first entry)
DE cDNA sequence #572 encoding novel human secreted protein.
EE
EX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW immunosuppressive; antirheumatic; ss.
XX
OS Homo sapiens.
XX
XX WO200177291-A2.
XX
XX 18-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-US10485.
XX
XX 06-APR-2000; 2000US-195604P.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Wong GG, Clark HF, Fechtel K, Agostino MU, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX
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DR WPI; 2002-010900/01.
XX
PT New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease -
XX
XX Claim 1; Page 363-364; 391pp; English.
PS
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC The polynucleotide sequences of the invention are also useful in gene
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC invention that encode for novel human secreted proteins.
XX
SQ Sequence 1616 BP; 369 A; 503 C; 441 G; 298 T; 5 other;
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Query Match 85.8%; Score 1145; DB 24; Length 1616;
Best Local Similarity 90.8%; Pred. No. 3.4e-214;
Matches 1242; Conservative 0; Mismatches 93; Indels 33; Gaps 1;
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QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
Db 123 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGTATACAAACAGGCGGTCCCTGAGACTC 182
QY 61 TCCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGTGATGCTCGGTCCGCGAGCT 120
Db 193 TCCTGCACAGGTTCTGGATTCCTCGTTGGTGATTTATGGTGTGAGCTGGTCCGCGAGCT 242
QY 121 CCAGGAAGGGGCTCGAGTGGGTTGCTGAAATAGATTGAATCTGAAATCTGATAATTATGCAACA 180
Db 243 CCAGGAAGGGGCTGGAGTGGGTAGGCTCAATGAGACCGAGGCTTATGGTGGGACAAGA 302
QY 181 CATATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 303 AATTACGCCGCTCTGTGACGGGCGAGATTACCATCTCAAGAGATGATTCAAAAGCCATC 362
QY 241 CTGTATCTGCAAAATGAACAGCTTGAAACCCGAGGACACAGCGCTGTATTACTGTA----- 295
Db 363 GCCTATCTGCAAGTGAAGAGCTTGAAACCCGAGGACACAGCGCTTTATCACTGTAGTAA 422
QY 296 -----CAGATTTCATAGACTGGGGCCAGGGGAACACTA 327
Db 423 CATTAATAATGATGATCTGTTATCAGCAATACTTCCAAACACTGGGGGAGGCAACCTG 482
QY 328 GTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCC 387
Db 483 GTCATCTGCTCTCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCC 542
QY 388 AAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAA 447
Db 543 AAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAA 602
QY 448 CCGGTGACGGTGTGCGTGAACACTAGGGCCCTGACACAGCGGCTGCACACTTCCCGGCT 507
Db 603 CCGGTGACGGTGTGCGTGAACACTAGGGCCCTGACACAGCGGCTGCACACTTCCCGGCT 662
QY 508 GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGC 567
Db 663 GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCAGCAGC 722
QY 568 TTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCCCAACACCAAGGTGGAC 627
Db 723 TTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCCCAACACCAAGGTGGAC 782
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Qy	430	AAGACTACTTCCCAGAACCGGTGACGGTGTCGTGGAACCTCAGCGCCCTTGACCAGCGGC	489
Db	481	AAGGACTACTTCCCCAAGCCGTGACGGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGC	540
Qy	490	GTCACACACTTCCCGGCTGCTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG	549
Db	541	GTGCACACACTTCCCGGCTGCTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG	600
Qy	550	ACCGTGCCCTCCACGAGCTTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAAGCC	609
Db	601	ACCGTGCCCTCCACGAGCTTGGGCACCCAGACCTACATCTGCAAGCTGAATCACAAAGCC	660
Qy	610	AGCAACACCAAGGTGGACAGAAGATGGAGGCCAAATCTTTGTGACAAAACCTCACACATGC	669
Db	661	AGCAACACCAAGGTGGACAGAAGATGGAGGCCAAATCTTTGTGACAAAACCTCACACATGC	720
Qy	670	CCACGTCGCCAGCACCTCAACTCGCGGGGGACCGTCAGTCTTCTCTCCCCCCAAAA	729
Db	721	CCACGTCGCCAGCACCTCAACTCTTGGGGGACCGTCAGTCTTCTCTCCCCCCAAAA	780
Qy	730	CCCAAGCACACCCCTCATGATCTCCGGGACCCCTGAGGTACATCGTGGTGGTAGCGTG	789
Db	781	CCCAAGCACACCCCTCATGATCTCCGGGACCCCTGAGGTACATCGTGGTGGTAGCGTG	840
Qy	790	AGCCAGAGAACCCTTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATAAT	849
Db	841	AGCCAGAGAACCCTTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATAAT	900
Qy	850	GCCAAGACAAGCCGGGAGGAGCAGTACACAGCAGCTACCGTGTGGTGCAGGTCCTC	909
Db	901	GCCAAGACAAGCCGGGAGGAGCAGTACACAGCAGCTACCGTGTGGTGCAGGTCCTC	960
Qy	910	ACCGTCTGTCAACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGGTCTCCAACAAA	969
Db	961	ACCGTCTGTCAACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGGTCTCCAACAAA	1020
Qy	970	GCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCGAGCCCGAGAACCA	1029
Db	1021	GCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCGAGCCCGAGAACCA	1080
Qy	1030	CAGGTGTACACCTGCCCCCATCCGGGATGAGTGCACCAAGACAGGTGAGCTGACC	1089
Db	1081	CAGGTGTACACCTGCCCCCATCCGGGATGAGTGCACCAAGACAGGTGAGCTGAGC	1140
Qy	1090	TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGCTGGAGTGGGAGACGAATGGGCG	1149
Db	1141	TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGCTGGAGTGGGAGCAATGGGCG	1200
Qy	1150	CCGAGAACCAACTACAGACCAAGCCCTCCGTGTGGACTCGAGCGGTCTCTTCTGCTC	1209
Db	1201	CCGAGAACCAACTACAGACCAAGCCCTCCGTGTGGACTCGAGCGGTCTCTTCTGCTC	1260
Qy	1210	TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGAAGTCTTCTCATGTCC	1269
Db	1261	TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGAAGTCTTCTCATGTCC	1320
Qy	1270	GTGATGATGAGGCTGTGCACCAACCACTACACGCGAGAAGAGCTCTCCCTGTCCGGGT	1329
Db	1321	GTGATGATGAGGCTGTGCACCAACCACTACACGCGAGAAGAGCTCTCCCTGTCCGGGT	1380
Qy	1330	AAATGA 1335	
Db	1381	AAATGA 1386	

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RESULT 10
AAC84205
ID ID AAC84206 standard; DNA; 6281 BP.
XX XX
AC AC AAC84206;
XX XX
DT DT 19-MAR-2001 (first entry) .
XX XX

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DE	Plasmid Glambda-lapcd DNA sequence.
XX	
KW	Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW	Glambda-1; human; virucide; RSV propagation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200069462-A1.
XX	
PD	23-NOV-2000.
XX	
PF	18-MAY-2000; 2000WO-US13694.
XX	
PR	18-MAY-1999; 99US-0134702.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Gross MS, Sweet RW, Taylor G;
XX	
DR	WPI; 2001-024947/03.
XX	
PT	Human monoclonal antibody and functional fragments, useful for
PT	therapeutic and/or prophylactic treatment of respiratory syncytial
PT	virus infection, is specifically reactive with the F protein epitope of
PT	the virus -
XX	
PS	Claim 6; Fig 8A-F; 102pp; English.
XX	
CC	The invention provides a human monoclonal antibody (I) and its functional
CC	fragments specifically reactive with an F protein epitope of respiratory
CC	syncytial virus (RSV), and capable of neutralizing infection by the virus
CC	such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC	standard recombinant methodology. (I) is useful for detecting RSV by
CC	contacting a source suspected of containing RSV with (I) and determining
CC	whether (I) binds to the source. (I) is also useful for providing passive
CC	immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC	for therapeutic and/or prophylactic treatment of RSV infection in human
CC	patients, particularly infants and young children. (I) is also useful
CC	as a diagnostic reagent for the determination of RSV mediated disorders
CC	or for tracking progress of treatment of the disorders. The present
CC	sequence represents the continuous DNA sequence of the expression plasmid
CC	Glambda-laped containing the RSV neutralising human Glambda-1 mAb for the
CC	heavy chain.
XX	
SQ	Sequence 6281 BP; 1555 A; 1634 C; 1618 G; 1474 T; 0 other;
	Query Match 85.6%; Score 1142.8; DB 22; Length 6281;
	Best Local Similarity 91.6%; Pred. No. Ie-213;
	Matches 1242; Conservative 0; Mismatches 87; Indels 27; Gaps 21;
Qy	1 GAGGTGCACGCTGGTGGAGCTCTGGGGAGCGCTTGTFAAAGCCGGGGCGTCCTTTAGACTC 60
Db	1072 GAGGTCCAATGCTCGAGTCTGGGGAGCGCTTGTTACAGCCTGGGGGTGCCCTGAGACTC 1131
Qy	61 TCCTGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTCGATCTCCTGGTCCGCCAGGCT 120
Db	1132 TCCTGCGCAGCCTCTGGAGTCTCCCTCAGTGGATACAAGATGAACCTGGTCCGCCAGGCT 1191
Qy	121 CCAGGGAAGGGCTCGAGTGGTGTCTGAAATTAGATTGAATCTGTAATTATTCACACA 180
Db	1192 CCAGGGAAGGGCTGGAAATGGGTCTCTTCCATT-----ACTGGTATGAGTAATTACATA 1245
Qy	181 CATATCGGAGTCTGTCAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db	1246 CACTACTCAGACTCAGTGAAGGGCGATTCCACATCTCCAGAGAACCGCATGAACCTCA 1305
Qy	241 CTGTATCTGCAAAATGAACAGCCTGAAAAACCGAGGACACAGCGCTGTATTACTGT ----- 294
Db	1306 CTGTATCTGCAAAATGAACAGCCTGACACCCGANGACACGGGTGTTATTATTGTCGGACA 1365
Qy	295 -----ACAGATTTTCATAGACTGGGCCCGAGGGAACACTAGTCACCGCTTCC 339
Db	1366 CAACCGGGGAGCTGGGSCCTTTGAOCCATTGGGGCCAGGGAACCCCTGTGTCACCGTCTCC 1425

Qy	340	TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACACCTCTCTCCAAGACGACCTCT	399
Db	1426		
		TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACACCTCTCTCCAAGACGACCTCT	1485
Qy	400	GGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTG	459
Db	1486		
		GGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTG	1545
Qy	460	TCGTGGAACTCAGGGGCCCTGACACGGCGGTGCACACTTCCCGGTGTGCTTACAGTCC	519
Db	1546		
		TCGTGGAACTCAGGGGCCCTGACACGGCGGTGCACACTTCCCGGTGTGCTTACAGTCC	1605
Qy	520	TCAGGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGCAGCTTGGGACACCCAG	579
Db	1606		
		TCAGGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGCAGCTTGGGACACCCAG	1665
Qy	580	ACCTACATCTGCAACCTGTAATCACAAAGCCCAACCAAGGTGGACAAAGAAAGTGGAG	639
Db	1666		
		ACCTACATCTGCAACCTGTAATCACAAAGCCCAACCAAGGTGGACAAAGAAAGTGGAG	1725
Qy	640	CCCAAACTTGTGACAAACTCACATGCCACCGTCCCGACGACCTGAACTCGCGGGG	699
Db	1726		
		CCCAAACTTGTGACAAACTCACATGCCACCGTCCCGACGACCTGAACTCCTGGG	1785
Qy	700	GCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGTATCTCCCGGACC	759
Db	1786		
		GGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGTATCTCCCGGACC	1845
Qy	760	CCTGAGGTACATGCGTGGTGGTGGACGTGACGCACGAAGACCCCTGAGGTCAAGTTCAAC	819
Db	1846		
		CCTGAGGTACATGCGTGGTGGTGGACGTGACGCACGAAGACCCCTGAGGTCAAGTTCAAC	1905
Qy	820	TGGTACCTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTAC	879
Db	1906		
		TGGTACCTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTAC	1965
Qy	880	AACAGCAGTACCGTGTGGTTCAGGCTCTCACCCTCTGCAACAGGACTGGCTGGAATGGC	939
Db	1966		
		AACAGCAGTACCGGTTGGTTCAGGCTCTCACCCTCTGCAACAGGACTGGCTGGAATGGC	2025
Qy	940	AAGGAGTACAAGTGCAAGGCTCTCAACAAAGCCCTCCACAGCCCTCCAGAGGAGTCAAC	999
Db	2026		
		AAGGAGTACAAGTGCAAGGCTCTCAACAAAGCCCTCCAGAGGAGTCAAC	2085
Qy	1000	TCCAAAGCCAAAGGGACGCCCGAGAACACAGGTGTACACCCCTGCCCCCATCCCGGAT	1059
Db	2086		
		TCCAAAGCCAAAGGGACGCCCGAGAACACAGGTGTACACCCCTGCCCCCATCCCGGAT	2145
Qy	1060	GAGCTGACCAAGAACCAGGTTCAGCTGACCTGCCTGGTCAAGGCTTCTATCCGAGGCAC	1119
Db	2146		
		GAGCTGACCAAGAACCAGGTTCAGCTGACCTGCCTGGTCAAGGCTTCTATCCGAGGCAC	2205
Qy	1120	ATCGCCCTGGAGTGGGAGAGCAATGGCGAGCCGAGAGAACACTACAAGACCAAGCTCC	1179
Db	2206		
		ATCGCCCTGGAGTGGGAGAGCAATGGCGAGCCGAGAGAACACTACAAGACCAAGCTCC	2265
Qy	1180	GTGCTGGACTCCAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCGAGG	1239
Db	2266		
		GTGCTGGACTCCAGCGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAGAGCGAGG	2325
Qy	1240	TGGCAGCAGGGGAACCTCTTCTCATGCTCCGTTGATGATGAGGCTCTGCAACACCACTAC	1299
Db	2326		
		TGGCAGCAGGGGAACCTCTTCTCATGCTCCGTTGATGATGAGGCTCTGCAACACCACTAC	2385
Qy	1300	ACGCAGAGAGGCTCTTCCCTGTCTCCGGGTAAATGA	1335
Db	2386		
		ACGCAGAGAGGCTCTTCCCTGTCTCCGGGTAAATGA	2421

RESULT 11
AAV61794
ID AAV6

Query Match		85.5%;	Score 1141.8;	DB 19;	Length 1427;
Best Local Similarity		91.6%;	Pred. No. 1.4e-213;		
Matches 1241;		Conservative	0;	Mismatches	87; Indels 27; Gaps 2;
Qy	2	AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT	61		
Db	71	AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT	130		
Qy	62	CTGTGCAGCTAGCGGATTCATTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCTC	121		
Db	131	CGTGTGCAGCTCTGGAAACCCCTCAGTGGCTATACCATGCACTGGGTCCGCCAGGCTC	190		
Qy	122	CAGGGAAGGGCTCGAGTGGTGTGCTGAAATAGATTTCAATTCGATAATATGCAACAC	181		
Db	191	CAGGGAAGGGCTCGAGTGGTGTGCTGAAATAGATTTCAATTCGATAATATGCAACAC	244		
Qy	182	ATTATGGCGAGTCTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC	241		
Db	245	AATACTCAGACTCAGTGAAGGGCGGATTCACCATCTCCAGAGACAAGCCCAAGAACTCAC	304		
Qy	242	TGTATCTCAATGAACAGCCTGAAACCCGAGGACAGACGCTGTATTACTGT-----	294		
Db	305	TTTATCTCAATGAACAGCCTGACAGCCGAGGACAGGCTGTCTATTATTGTGCGACCG	364		
Qy	295	-----ACAGATTTCTAGACTGGGGCCAGGGAACTAGTCAACCGTCTCCT	340		
Db	365	CCCTATATAGCACCGCCTTACTTTGACCACCTGGGGCCAGGAAACCCCTGTCACCGTCTCCT	424		
Qy	341	CAGCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGACCGCTCTCCCAAGAGCACCTCTG	400		
Db	425	CAGCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGACCGCTCTCCCAAGAGCACCTCTG	484		
Qy	401	GGGGCACAGCGCCCTGGGCTGCCTGTGTCAGGACTACTTCCCGCAACCGGTGACGGTGT	460		
Db	485	GGGGCACAGCGCCCTGGGCTGCCTGTGTCAGGACTACTTCCCGCAACCGGTGACGGTGT	544		
Qy	461	CGTGAATCTCAGGCGCCTGACAGCGCGGTGACACCGTTCGCCGGCTGCTCAGACTCT	520		
Db	545	CGTGAATCTCAGGCGCCTGACAGCGCGGTGACACCGTTCGCCGGCTGCTCAGACTCT	604		
Qy	521	CAGGACTCTACTTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGA	580		
Db	605	CAGGACTCTACTTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGA	664		
Qy	581	CCTACATCTGCAAGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTGAGC	640		
Db	665	CCTACATCTGCAAGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC	724		
Qy	641	CCAATCTTGTGACAAACTCACACATGCCACCGTGCCCGAGCACCTGAACTCCGCGGGG	700		
Db	725	CCAATCTTGTGACAAACTCACACATGCCACCGTGCCCGAGCACCTGAACTCCGCGGGG	784		
Qy	701	CACCGTCACTCTTCTCTTCCCGCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCC	760		
Db	785	GACCGTCACTCTTCTCTTCCCGCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCC	844		
Qy	761	CTGAGGTCAATGCGTGGTGGACGTGACGCCACGAAGACCCCTGAGTCAAGTTCAACT	820		
Db	845	CTGAGGTCAATGCGTGGTGGACGTGACGCCACGAAGACCCCTGAGTCAAGTTCAACT	904		
Qy	821	GGTACGTGGAGCGCTGAGGTGCAATATGCCAAGACAAAGCCCGGAGGAGCAGTACA	880		
Db	905	GGTACGTGGAGCGCTGAGGTGCAATATGCCAAGACAAAGCCCGGAGGAGCAGTACA	964		
Qy	881	ACAGCACGTACCGTGGTGCAGCGTCTTCAACCGTCTGACCCAGGACTGGCTGAATGGCA	940		
Db	965	ACAGCACGTACCGGCTGGTGCAGCGTCTTCAACCGTCTGACCCAGGACTGGCTGAATGGCA	1024		
Qy	941	AGGAGTACAAAGTGCAGGCTCTCCCAACAAGCCCTCCAGCCGCCCATCGAGAAACCATCT	1000		
Db	1025	AGGAGTACAAAGTGCAGGCTCTCCCAACAAGCCCTCCAGCCGCCCATCGAGAAACCATCT	1084		

Qy	1001	CCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCCGGGATG	1060
Db	1085	CCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCCGGGATG	1144
Qy	1061	AGCTGACCAAGAACAGGTCAGCCTGACCTGCTGTGTCAAAGGCTTCTATCCACGCGACA	1120
Db	1145	AGCTGACCAAGAACAGGTCAGCCTGACCTGCTGTGTCAAAGGCTTCTATCCACGCGACA	1204
Qy	1121	TCGCCCTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAGACACCGCTCCCG	1180
Db	1205	TCGCCCTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAGACACCGCTCCCG	1264
Qy	1181	TGCTGACCTCCGACGGCTCCTTCTCTCTACAGCAAGCTACCGTGGACACAGCAGGT	1240
Db	1265	TGCTGACCTCCGACGGCTCCTTCTCTCTACAGCAAGCTACCGTGGACACAGCAGGT	1324
Qy	1241	GGCAGCAGGGGAGCGTCTTCTCATGCTCGTGTATGATGATGAGCTCTGCACAACCACTACA	1300
Db	1325	GGCAGCAGGGGAGCGTCTTCTCATGCTCGTGTATGATGATGAGCTCTGCACAACCACTACA	1384
Qy	1301	CGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1335
Db	1385	CGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1419
RESULT 14			
AAV41429			
ID	AAV41429 standard; DNA; 1427 BP.		
AC	AAV41429;		
DT	12-OCT-1998 (first entry)		
DE	Plasmid Hu19BHcpd encoding anti-Rsv F protein Hu19B heavy chain.		
KW	Monoclonal antibody; human; Hu19B; engineered antibody; RSV;		
KW	respiratory syncytial virus; complementarity determining region;		
OS	Homo sapiens.		
FH	Key		
FT	Location/Qualifiers		
FT	13..1419		
FT	/*tag= a		
PN	W09819704-AL.		
PD	14-MAY-1998.		
PF	23-OCT-1997; 97WO-US19203.		
PR	01-NOV-1996; 96US-0030149.		
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PI	Deen KC, Dillon SB, Porter TG, Sweet RW;		
XX	WPI; 1998-286600/25.		
DR	P-PSDB; AAW59625 and AAW59628.		
XX	Monoclonal antibodies reactive with Respiratory Syncytial Virus -		
PT	useful for detection, prevention and treatment of RSV infections		
XX	Example B; Fig 4C; 109pp; English.		
CC	This is the DNA sequence of plasmid Hu19BHcpd, which includes a		
CC	coding region for anti-respiratory syncytial virus (RSV) fusion		
CC	(F) protein human monoclonal antibody (MAb) Hu19B heavy chain (see		
CC	also AAW59616). Hu19BLcpn (see AAV41430) encoding the Hu19B light		
CC	chain is also provided. These vectors were used to produce Hu19B		
CC	in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19D		
CC	MAbs are claimed. These are reshaped human antibodies comprising a		
CC	heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and		

CC a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).
CC These are neutralising engineered antibodies that inhibit virus
CC growth in vitro and in vivo in animal models of RSV infection.
CC They can be used in the detection, prevention and passive
CC immunotherapy of RSV infection. Nucleic acids encoding the human
CC MAb, recombinant plasmids (see AAV41427-33) and host cells are
CC provided.

XX
SQ Sequence 1427 BP; 325 A; 461 C; 382 G; 259 T; 0 other;

Query Match 85.48; Score 1140.2; DB 19; Length 1427;
Best Local Similarity 91.5%; Pred. No. 2.9e-213;
Matches 1240; Conservative 0; Mismatches 86; Indels 27; Gaps 2;
2 AGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
DB 71 AGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTCAAGGCTGGCGGGTCCCTAAGACTCT 130
QY 62 CTTGTGAGCTAGCGATTCACTTTTCAGTGGTACTGGATGCTCTGGTCCGCCAGGCTC 121
DB 131 CTTGTGAGCTAGCGATTCACTTTTCAGTGGTACTGGATGCTCTGGTCCGCCAGGCTC 190
QY 122 CAGGGAAGGGCTCGAGTGGTGGTGAATAGATTGAATCTGATTAATGCAACAC 181
DB 191 CAGGGAAGGGCTCGAGTGGTGGTGGTCAATTTCAATTTCAATTTCAATTTCAATTT 244
QY 182 ATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
DB 245 ACTACTCAGACTCAGTGAAGGCGGATTCCACCATCTCCAGAGACAAAGCCAGAACTCNC 304
QY 242 TGTATCTGCAATGAACACGCTTGAACACCGAGGACACAGCGCTGATTACTGT----- 294
DB 305 TTATCTGCAATGAACACGCTTGAACACCGAGGAGACAGCGCTGATTACTGTGGGACCG 364
QY 295 -----ACAGATTTCATAGACTGGGCGCAGGAACTAGTACCCGCTCTCT 340
DB 365 CCCCTATACACGCGCTTACTTTGACCACTGGGGCGAGGAACCTTGGTACCGCTCTCT 424
QY 341 CAGCCTCCACCAAGGCCCATCGGTCTTCCCTCGCAGCCCTCCCTCCAGAGCACTCTG 400
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QY 401 GGGGACACGCGCTGGGCTGGCTGCTCAAGGACTACTTCCCGAAGCGGTGACGGTGT 460
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QY 461 CTTGGAACCTCAGCGGCTTGAACAGCGGTGCACACCTTCCCGGCTGTCTTACAGTCT 520
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DB 605 CAGGACTCTACTCTCAGCAGCGGTGGTACCGTGGCTTCCAGCAGCTTGGGACCCAGA 664
QY 581 CTTACATCTGCAAGTGAATCAAGCCAGCCAGCAACACCAAGTGGACAAAGTGGAGC 640
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QY 641 CCAAAATCTTGTGACAAAATCAACATGCCACCGTGGCCAGCAGCTGAACCTCGCGGGG 700
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QY 881 ACAGCACCTACCGTGTGGTCAAGGCTCTCAGCGTCTCCAGCAGGACTGGCTGAATGGCA 940
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QY 1181 TGCTGGAGTCCGAGCGGCTCTTCTCTCATGCTCCGCTGATGATGATGATGATGATGAT 1240
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RESULT 15

AAS62784
ID AAS62784 standard; cDNA; 1617 BP.

XX AC AAS62784;

XX DT 14-FEB-2002 (first entry)

XX DE cDNA sequence #571 encoding novel human secreted protein.

XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX KW immune deficiency disorder; blood disorder; inflammatory disorder;
XX KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
XX KW immunosuppressive; antirheumatic; ss.

XX OS Homo sapiens.

XX PN WO200177291-A2.

XX PD 18-OCT-2001.

XX PF 29-MAR-2001; 2001WO-US10485.

XX PR 06-APR-2000; 2000US-195604P.

XX PA (GENY) GENETICS INST INC.

PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;

DR WPI; 2002-010900/01.

XX New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease -

XX PS Claim 1; Page 363; 391pp; English.

CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 129.024 Seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716b-18
Perfect score: 1335
Sequence: 1 gaggtgagctgtgtgagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubnpa/US09_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1147.8	86.0	1798	9 US-09-925-299-230	Sequence 230, App
2	1147.8	86.0	1798	10 US-09-925-299-230	Sequence 230, App
3	1147.2	85.9	1437	9 US-10-124-905-7	Sequence 7, Appli
4	1147.2	85.9	1437	9 US-09-948-429B-7	Sequence 7, Appli
5	1147.2	85.9	1437	9 US-10-073-138-4	Sequence 4, Appli
6	1145	85.8	1616	10 US-09-822-830A-572	Sequence 572, App
7	1141.8	85.5	1427	12 US-10-066-895-25	Sequence 25, Appl
8	1141.8	85.5	1427	12 US-10-066-895-27	Sequence 27, Appl
9	1140.2	85.4	1427	12 US-10-066-895-20	Sequence 20, Appl
10	1136.6	85.1	1617	10 US-09-822-830A-571	Sequence 571, App
11	1135	85.0	1347	10 US-09-736-371B-20	Sequence 20, Appl
12	1131	84.7	1356	10 US-09-822-698A-27	Sequence 27, Appl
13	1128.8	84.6	6284	12 US-10-066-895-14	Sequence 14, Appl
14	1121.4	84.0	9182	9 US-09-927-122-41	Sequence 41, Appl
15	1105.2	82.8	1598	10 US-09-822-849A-103	Sequence 103, App
16	1104.8	82.8	1404	10 US-09-825-012-10	Sequence 10, Appl
17	1102.2	82.6	2196	10 US-09-825-012-44	Sequence 44, Appl
18	1102.2	82.6	2196	10 US-09-825-012-45	Sequence 45, Appl
19	1102.2	82.6	2226	10 US-09-825-012-53	Sequence 53, Appl

20	1102.2	82.6	2226	10 US-09-825-012-54	Sequence 54, Appl
21	1100	82.4	1590	10 US-09-822-849A-114	Sequence 114, App
22	1096.6	82.1	2190	10 US-09-825-012-50	Sequence 50, Appl
23	1096.6	82.1	2190	10 US-09-825-012-51	Sequence 51, Appl
24	1096.6	82.1	2220	10 US-09-825-012-59	Sequence 59, Appl
25	1096.6	82.1	2220	10 US-09-825-012-60	Sequence 60, Appl
26	1095.8	82.1	2193	10 US-09-825-012-47	Sequence 47, Appl
27	1095.8	82.1	2193	10 US-09-825-012-48	Sequence 48, Appl
28	1095.8	82.1	2223	10 US-09-825-012-56	Sequence 56, Appl
29	1095.8	82.1	2223	10 US-09-825-012-57	Sequence 57, Appl
30	1088	81.5	3300	9 US-10-020-786-1	Sequence 1, Appli
31	1086	81.3	3300	9 US-10-020-786-2	Sequence 2, Appli
32	1082.6	81.1	8120	9 US-09-726-258-68	Sequence 68, Appl
33	1082	81.0	4207	10 US-09-897-006-4	Sequence 4, Appli
34	1082	81.0	5732	10 US-09-897-006-6	Sequence 6, Appli
35	1077.6	80.7	1615	10 US-09-822-849A-111	Sequence 111, App
36	1077.6	80.7	1615	10 US-09-822-830A-303	Sequence 303, App
37	1075.8	80.6	1634	10 US-09-822-830A-307	Sequence 307, App
38	1073	80.4	1576	10 US-09-822-849A-321	Sequence 321, App
39	1067.8	80.0	1640	10 US-09-822-849A-321	Sequence 321, App
40	1064.4	79.7	4210	10 US-09-897-006-5	Sequence 5, Appli
41	1064	79.7	1565	10 US-09-822-849A-241	Sequence 241, App
42	1061.4	79.5	1643	10 US-09-822-830A-302	Sequence 302, App
43	1057.6	79.2	1565	10 US-09-822-849A-104	Sequence 104, App
44	1050.6	78.7	1449	10 US-09-747-669-1	Sequence 1, Appli
45	1050.6	78.7	1449	10 US-09-747-669-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-925-299-230

Sequence 230, Application US/0925299

Publication No. US20030040617A9

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 230

LENGTH: 1798

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (15)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (24)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (31)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (501)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (1798)

OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-230

Query Match

86.0%; Score 1147.8; DB 9; Length 1798;

	Best Local Similarity	91.08%; Pred. No. 4e-311;	Matches 1245; Conservative	10; Mismatches	73; Indels	40; Gaps	2;
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Db	206	AGGTGACGCTGGTGAGTCTGGGGAGGCGTGGTCCAGCGTGGAGGTCCCTGAGACTCT	265				
QY	62	CTGTGTGACGTAGCGGATTCATTTTCAGTGCTACTGGATGTCCTGGTCCGCCAGGCTC	121				
Db	266	CTGTGTGACGCTCTGGATTCACCTTCAGTAGCTATGGCATGSCATGGTGGCCGACGGCTC	325				
QY	122	CAGGGAAGGGCTCAGGTGGTGTGCTGAAATAGATTGAAATCTGATAATATGCAACAC	181				
Db	326	CAGGGAAGGGCTGAGGTGGTGGCAGTTATATATATATATATATATATATATATATAT	379				
QY	182	ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC	241				
Db	380	ACTATGCACATCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCAGAAACACGC	439				
QY	242	TGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCGGTGTTATTACTGTACAGATT	301				
Db	440	TGTATCTGCAATGAACAGCCTGAGAGCTGAGGACAGCGGTGTTATTACTGTGCGARAG	499				
QY	302	TCAT-----AGACTGGGGCCAGGAAACACTA	327				
Db	500	ANGTTACTATGTTTCGAAAGCATCTACTACTTTGACTCTGGGGCCAGGAAACMCTG	559				
QY	328	GTACACGCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGTCGACACCTCCTCC	387				
Db	560	GTACACGCTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGTCGACACCTCCTCC	619				
QY	388	AAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTGTCAGGACTACTTCCCGCAA	447				
Db	620	AAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTGTCAGGACTACTTCCCGCAA	679				
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Db	680	CCGGTGACGGTGTGTGGAACTCAGCGCCCTGACAGCGCGCTGCACACTTCCCGGCT	739				
QY	508	GTCTTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGCTCCACGACG	567				
Db	740	GTCTTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACGCTCCACGACG	799				
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Db	800	TTGGGCACCCAGACTTACATCTGCAACGTGAATCAGAGCCCGACACACCAAGTTGGAC	859				
QY	628	AAGAAAGTGAGCGCCAAATTTGTGACAAAACCTCACATGCCACCGTGCACAGACCT	687				
Db	860	AAGAAAGTGAGCGCCAAATTTGTGACAAAACCTCACATGCCACCGTGCACAGACCT	919				
QY	688	GAATCTCGGGGGCACCGTCAGTCTTCCTCTTCCCGCCAAACCCAAAGACACCTCATG	747				
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QY	748	ATCTCCGGGACCCCTCAGGTTCACATGCTGTGGTGGACGTGAGCCAGAGACCCCTGAG	807				
Db	980	ATCTCCGGGACCCCTCAGGTTCACATGCTGTGGTGGACGTGAGCCAGAGACCCCTGAG	1039				
QY	808	GTCAAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATTAATGCCAAGACAAGCCCGG	867				
Db	1040	GTCAAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATTAATGCCAAGACAAGCCCGG	1099				
QY	868	GAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCGTCTCAACGCTCTGCACAGGAC	927				
Db	1100	GAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCGTCTCAACGCTCTGCACAGGAC	1159				
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QY	1048	CCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGCCTGGTGAAGAGGTTTC	1107
Db	1280	CCATCCCGGGAGAGMTGACCAAGAACCAGGTGACCTGCCTGGTCAAAAGGTTTC	1339
QY	1108	TATCCAGCGACATCCCGCTGAGTGGGAGAGCAATGGCAGCGGAGAACCACTACAAG	1167
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QY	1228	GACAAGACAGGTGGCAGCAGGAGGAACTCTTCTCATGCTCCGTGATCATGAGGCTCTG	1287
Db	1460	GACAAGACAGGTGGCAGCAGGAGGAACTCTTCTCATGCTCCGTGATCATGAGGCTCTG	1519
QY	1288	CACAACCACTACACGAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA	1335
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RESULT 2			
US-09-925-299-230			
; Sequence 230, Application US/09925299			
; Patent No. US20020055627A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			
; FILE REFERENCE: PA102			
; CURRENT APPLICATION NUMBER: US/09/925,299			
; CURRENT FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: PCT/US00/05883			
; PRIOR FILING DATE: 2000-03-08			
; PRIOR APPLICATION NUMBER: 60/124,270			
; PRIOR FILING DATE: 1999-03-12			
; NUMBER OF SEQ ID NOS: 1556			
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; ORGANISM: Homo sapiens			
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; OTHER INFORMATION: n equals a,t,g, or c			
US-09-925-299-230			

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Query Match									
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QY	61	TCCTGTGACAGTAGCGGATTCACCTTCAGTGGCTACTGGATGCTCGTGGTCCGCGAGGCT	120						
DB	118	TCCTGTGACAGTCTCTGGATTCACCTTCAGTGACCACTACATGATTGGTTCGCGCAGGCT	177						
QY	121	CCAGGGAAGGGGCTCGAGTGGTGGTGAATTTAGATTGAAATCTGATAAATTTATCAACA	180						
DB	178	CCAGGGAAGGGGCGGAATGGGTAGGTTTCATTAGAAACAAACCGGTGGGACAACA	237						
QY	181	CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA	240						
DB	238	GAATAGCGCGCTGTGTGAAGACAGATTCACCATCTCCAGAGATGATTCACAAAGCATC	297						
QY	241	CTGTATCTCAAAATGAACAGCCTGAAACCCGAGGACACAGCGCTGATTACTGTAC----	296						
DB	298	GCTATCTCAATGAGCAGCCTGAAATCGAGGACCGGCGCTCTATTCTGTACTACA	357						
QY	297	-----AGATTTTCATAGACTGGGC	315						
DB	358	TCCTACATTTACATTTGTCGGGTGGTGTCTGCTATGAGGTTTACTTCGAATTTCTGGGC	417						
QY	316	CAGGGAACACTAGTACCGTCTCCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTG	375						
DB	418	CAGGGCGCCTGGTCACCGTCTCCCTCAGCTAGCAGCAAGGGCCCATCGGTCTTCCCGCTG	477						
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QY	496	ACCTTCCCGGCTGCTCTCAGTCTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTG	555						
DB	598	ACCTTCCCGGCTGCTCTCAGTCTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTG	657						
QY	556	CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAACAGCCCAAGAC	615						
DB	658	CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAACAGCCCAAGAC	717						
QY	616	ACCAAGGTGGACAAGAGTGAGCGCCCAATCTTGTGACAAACTCAGCATGCCACCG	675						
DB	718	ACCAAGGTGGACAAGAGTGAGCGCCCAATCTTGTGACAAACTCAGCATGCCACCG	777						
QY	676	TGCCAGCACCTGAAGTCCGGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCCAAG	735						
DB	778	TGCCAGCACCTGAAGTCTCTGGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCCAAG	837						
QY	736	GACACCTCATGATCTCCCGGACCCCTGAGTGCATCATCGTGGTGGAGCGTGAGCCAC	795						
DB	838	GACACCTCATGATCTCCCGGACCCCTGAGGTGCATCATCGTGGTGGAGCGTGAGCCAC	897						
QY	796	GAAGACCTTGAGTCAAGTTCACCTGAGTGGAGCGCGTGGAGGTGCATTAATGCCAAG	855						
DB	898	GAAGACCTTGAGTCAAGTTCACCTGAGTGGAGCGCGTGGAGGTGCATTAATGCCAAG	957						
QY	856	ACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGAGCGTCTCACCGTC	915						
DB	958	ACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGAGCGTCTCACCGTC	1017						
QY	916	CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAAGCCCTC	975						
DB	1018	CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAAGCCCTC	1077						

QY	976	CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACACACAGGTG	1035
DB	1078	CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACACACAGGTG	1137
QY	1036	TACACCTTGCCTCCCATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCGCTG	1095
DB	1138	TACACCTTGCCTCCCATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCGCTG	1197
QY	1096	GTCAAGAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGACGCCGAG	1155
DB	1198	GTCAAGAGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGACGCCGAG	1257
QY	1156	AACAACACAAAGACACCGCTCCCGTGTGAGTCTCCAGCGCTCTCTTCTCTACAGC	1215
DB	1258	AACAACACAAAGACACCGCTCCCGTGTGAGTCTCCAGCGCTCTCTTCTCTACAGC	1317
QY	1216	AAGCTACCGTGGACAAAGAGAGAGTGGCAGAGGGGAACGTCTTCTCATGCTCCGTGATG	1275
DB	1318	AAGCTACCGTGGACAAAGAGAGAGTGGCAGAGGGGAACGTCTTCTCATGCTCCGTGATG	1377
QY	1276	CATGAGCTCTGCAACACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA	1335
DB	1378	CATGAGCTCTGCAACACCACTACACGACAGAGCGCTCTCCCTGTCTCCGGGTAAATGA	1437

RESULT 5

US-10-073-138-4
; Sequence 4, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,138
; FILING DATE: 13-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..1437
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-073-138-4

Query Match      85.9%; Score 1147.2; DB 9; Length 1437;
Best Local Similarity 90.7%; Pred. No. 5.5e-311;
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 58 GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCGTGGCGGGTCCCTGAGAGTC 117
QY 61 TCCTGTGACGCTAGCGGATTCACATTTTCAGTGGCTACTGATGCTCCGCGCCAGGCT 120
DB 118 TCCTGTGACGCTCTGGATTACACCTTCAGTGACCACTACATGATTGGTTCCGCGCCAGGCT 177
QY 121 CCAGGGAAGGGCTCGAGTGGTGGTCTGCAAAATTAGATTGAATCTGATTAATTGCAACA 180
DB 178 CCAGGGAAGGGCGGAATGGGTAGGTTTCATTAGAAACCAACCGCAACGGTGGGACAACA 237
QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 238 GAATACCGCGCTCTGTGAAGACAGATTTCACCATCTCCAGAGATGATTCCAAAGCATC 297
QY 241 CTGATCTGCAAAATGAACAGGCTGAAACCGGAGACACACCGGTGTAATTACTGTAC---- 296
DB 298 GCCTATCTGCAAAATGAGCAGCCTGAAAATCGAGACACGGCCGCTATTACTGTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
DB 358 TCCTACATTTCCAAATTTGCGGGGGTGGTGTCTGTATGAGAGGTACTCTCGAATTTCTGGGC 417
QY 316 CAGGGAACACTAGTACCGCTCTCTCAGCCTCCACCAAGGGCCCCATCGGTCTTCCGCCCTG 375
DB 418 CAGGGCGCCCTGGTACCGCTCTCCTCAGCTAGCAGCAAGGGCCCATCGGTCTTCCGCCCTG 477
QY 376 GCACCTCTCTCAAGAGACCTCTGGGGGACACAGCGGCCCTGGCTGCTTCAAGGAC 435
DB 478 GCACCTCTCTCAAGAGACCTCTGGGGGACACAGCGGCCCTGGCTGCTTCAAGGAC 537
QY 436 TACTTCCCGAACCCTGACGGTCTCTGGAACCTCAGCGGCCCTGACACAGCGCGGTGCAC 495
DB 538 TACTTCCCGAACCCTGACGGTCTCTGGAACCTCAGCGGCCCTGACACAGCGCGGTGCAC 597
QY 496 ACCTTCCCGGCTGCTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTG 555
DB 598 ACCTTCCCGGCTGCTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTG 657
QY 556 CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGAGCAAC 615
DB 658 CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGAGCAAC 717
QY 616 ACCAAGTGGACAAAGAGTGGAGCCCAAAATTTGTGACAAAACCTCACATGCCCCACCG 675
DB 718 ACCAAGTGGACAAAGAGAGAGCCCAAAATTTGTGACAAAACCTCACATGCCCCACCG 777
QY 676 TGCCCGACACCTGAACTGCGGGGGGACCGGTCACTTCTCTTCCCGCCCAAAACCCAAAG 735
DB 778 TGCCCGACACCTGAACTGCGGGGGGACCGGTCACTTCTCTTCCCGCCCAAAACCCAAAG 837
QY 736 GACACCCCTCATGATCTCCCGGACCCCTCAGGTACATCTGCGTGGTGGAGCTGAGCCAC 795
DB 838 GACACCCCTCATGATCTCCCGGACCCCTCAGGTACATCTGCGTGGTGGAGCTGAGCCAC 897
QY 796 GAAGACCCCTGAGGTCAAGTTCAACTGTTACGTGGACGCGCTGGAGGTGCATTAATGCCAAG 855
DB 898 GAAGACCCCTGAGGTCAAGTTCAACTGTTACGTGGACGCGCTGGAGGTGCATTAATGCCAAG 957
QY 856 ACAAGCCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGCGTCCCTACCGTC 915
DB 958 ACAAGCCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGCGTCCCTACCGTC 1017
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QY 916 CTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAAACAAAGCCCTC 975
DB 1018 CTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAAACAAAGCCCTC 1077
QY 976 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCAAAAGGCGAGCCCCGAGAACACAGGTG 1035
DB 1078 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCAAAAGGCGAGCCCCGAGAACACAGGTG 1137
QY 1036 TACACCTCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTGACCTGCGCTG 1095
DB 1138 TACACCTCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTGACCTGCGCTG 1197
QY 1096 GTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGGAGCCGAG 1155
DB 1198 GTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGGAGCCGAG 1257
QY 1156 AACAACTCAAGACACAGCGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1215
DB 1258 AACAACTCAAGACACAGCGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1317
QY 1216 AAGCTACCGTGGCAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGTCCGTGATG 1275
DB 1318 AAGCTACCGTGGCAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGTCCGTGATG 1377
QY 1276 CATGAGGCTCTGCACAACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAATGA 1335
DB 1378 CATGAGGCTCTGCACAACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAATGA 1437
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RESULT 6
US-09-822-830A-572
; Sequence 572, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalak
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 572
; LENGTH: 1616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1326,1377,1440,1579,1580
; OTHER INFORMATION: n=a,c,g, or t
US-09-822-830A-572
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Query Match      85.8%; Score 1145; DB 10; Length 1616;
Best Local Similarity 90.8%; Pred. No. 2.3e-310;
Matches 1242; Conservative 0; Mismatches 93; Indels 33; Gaps 1;

QY 1 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 123 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 182
QY 61 TCCTGTGACGCTAGCGGATTCATCTCACTGCTACTGATGCTCTGGTCCGCCAGGCT 120
DB 183 TCCTGTGACGCTAGCGGATTCATCTCACTGCTACTGATGCTCTGGTCCGCCAGGCT 242
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QY 121 CCAGGGAAGGGCTCGAGTGGTTCCTGAAATTAGATTGAATCTGATAATATATGCAACA 180
DB 243 CCAGGGAAGGGCTCGAGTGGTTCCTGAAATTAGATTGAATCTGATAATATATGCAACA 302
QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 303 AATTACGGCGCTGTGTGACGGCGAGATTCACCATCTCAAGAGATGATTCAAAAGCCATC 362
QY 241 CTGTATCTCAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTA----- 295
DB 363 GCCTATCTCAGATGACAGCTGAAACCGAGGACACAGCCCTTATCACTGTAGTAAA 422
QY 296 -----CAGTTTCATAGACTGGGCGGCGGGAACACTA 327
DB 423 CATTACTATGATGATACTGGTTATCAGCAATACTTCCAAACACTGGGCGGAGGCGACCGTG 482
QY 328 GTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCCTCCCTCC 387
DB 483 GTCATGCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCCTCCCTCC 542
QY 388 AAGAGCACCCTCTGGGGGACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAA 447
DB 543 AAGAGCACCCTCTGGGGGACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAA 602
QY 448 CGGTGACGGTGTCTGTGAACCTCAGCGCCCTGTGACCGCGCTGCACACCTTCCCGGCT 507
DB 503 CGGTGACGGTGTCTGTGAACCTCAGCGCCCTGTGACCGCGCTGCACACCTTCCCGGCT 662
QY 508 GTCCTACAGTCTCAGGACTCTACTCCTCAGCAGCGGTGGTACCGTGCCTCCAGCAGC 567
DB 663 GTCCTACAGTCTCAGGACTCTACTCCTCAGCAGCGGTGGTACCGTGCCTCCAGCAGC 722
QY 568 TTGGGACCCAGACCTTACATCTGCAAGCTGAATCAAGCCCGCAGCAACCAAGGTTGAC 627
DB 723 TTGGGACCCAGACCTTACATCTGCAAGCTGAATCAAGCCCGCAGCAACCAAGGTTGAC 782
QY 628 AAGAAAGTGAGCCCAATCTTGTGACAAACTCACATGCCACCGCTGCCAGCAGCCT 687
DB 783 AAGAGAGTTGAGCCCAATCTTGTGACAAACTCACATGCCACCGCTGCCAGCAGCCT 842
QY 688 GAACCTCGGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 747
DB 843 GAACCTCGGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 902
QY 748 ATCTCCCGGACCCCTGAGTGCATCTGCTGGTGGTGGAGCTGAGCCAGAGACCCCTGAG 807
DB 903 ATCTCCCGGACCCCTGAGTGCATCTGCTGGTGGTGGAGCTGAGCCAGAGACCCCTGAG 962
QY 808 GTCAAGTTCAACTGTGTGACGCGCTGGAGGTGCATATATGCCAAGCAAAAGCCGCGG 867
DB 963 GTCAAGTTCAACTGTGTGACGCGCTGGAGGTGCATATATGCCAAGCAAAAGCCGCGG 1022
QY 868 GAGGAGCAGTACACAGCAGCTACCGTGTGGTACGCTCTCACCGTCTGCACAGGAC 927
DB 1023 GAGGAGCAGTACACAGCAGCTACCGTGTGGTGGTGGAGCTGAGCCAGAGACCCAGGAC 1082
QY 928 TGCTGTAATGGCAGAGTACAGTGCAGAGTCTCCAAAGCCCTCCAGCCCGCCATC 987
DB 1083 TGCTGTAATGGCAGAGTACAGTGCAGAGTCTCCAAAGCCCTCCAGCCCGCCATC 1142
QY 988 GAGAAACCAATCTCCAAAGCCAGGCGCCGAGAACCAAGGCTGATACACCTGCGCC 1047
DB 1143 GAGAAACCAATCTCCAAAGCCAGGCGCCGAGAACCAAGGCTGATACACCTGCGCC 1202
QY 1048 CCATCCCGGAGTACGCTGACCAAGACAGGCTCAGCTGACCTGGTCTCAAGGCTTC 1107
DB 1203 CCATCCCGGAGGAGATGACCAAGAACCAAGGCTCAGCTGACCTGGTCTCAAGGCTTC 1262
QY 1108 TATCCAGCAGCATCGCGGTGGAGTGGAGAGCAATGGGACCGGAGAACCAACTACAG 1167
DB 1263 TATCCAGCAGCATCGCGGTGGAGTGGAGAGCAATGGGACCGGAGAACCAACTACAG 1322
QY 1168 ACCAGCGCTCCCGTGTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTACCGTG 1227

DB 1323 ACCNCGCTCCCGTCTGGACTCCGACGGTCTCTTCTCTATACCAAGCTCNCCTG 1382
QY 1228 GACAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGCTGATGATGAGGCTCTG 1287
DB 1383 GACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGCTGATGATGAGGCTNTG 1442
QY 1288 CACAACCACTACACGACGAGAAGCCTCTCCCTGTCTCCGGGTAATGA 1335
DB 1443 TTCAACCACTACACGACGAGAAGCCTCTCCCTGTCTCCCGGTAATGA 1490

RESULT 7

US-10-066-895-25
; Sequence 25, Application US/10066895
; Patent No. US20020141990A1

GENERAL INFORMATION:

APPLICANT: Deen, Keith C.
Dillon, Susan B.
Porter, Terence A.
Sweet, Raymond A.
TITLE OF INVENTION: Human Monoclonal Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19046

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/066,895
FILING DATE: 04-FEB-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/297,344

FILING DATE: 1999-JUN-09

APPLICATION NUMBER: 60/030,149

FILING DATE: 01-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Gelger, Kathleen
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: P50504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5968
TELEFAX: 610-270-5090
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 1427 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-10-066-895-25

Query Match

Best Local Similarity: 91.6%; Score 1141.8; DB 12; Length 1427;
Matches 1241; Conservative 0; Mismatches 87; Indels 27; Gaps 2;

QY 2 AGGTGAGCTGTGGAGCTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTCT 61

DB 71 AGGTGAGCTGTGGAGCTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTCT 130

QY 62 CTTGTCAGCTACGAGTTCACCTTTCAGTGGCTACTTGGATGCTCTGGGTCCGCCAGGCTC 121

DB 131 CGTGTGAGCCTCTGGAACCAACCTTCAGTGGCTATACCATGCACTGGGTCCGCCAGGCTC 190

Qy	122	CAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATAATATTGCAACAC	181
Db	191	CAGGGAAGGGGCTGGAGTGGGTCTCATCTT-----ACTGGAGGTAGCAACTTCATAA	244
Qy	182	ATTATCGGAGTCTGTGAAGGGGAAATTCAACATCTCAAGAGATGATTCAAATCTAGAC	241
Db	245	ACTACGACAGCTCAGTGAAGGGCCGATTCAACATCTCCAGAGACAACGCCAGAAGCTCAC	304
Qy	242	TGTATCTGCAAAATGAACAGCCTGAAACCCGAGGACACAGCCGTGTATTACTGT-----	294
Db	305	TTTATCTGCAAAATGAACAGCCTGACAGCCGAGGACACGGCTGTCTATTATTGTGCGACGG	364
Qy	295	-----ACAGATTTCATAGACTGGGCGCAGGAAACACTAGTCACCGTCTCT	340
Db	365	CCGCTATAGCACCGGCCCTACTTTGACCCTCTGGGCGCCAGGAAACCTGGTACCGTCTCT	424
Qy	341	CAGCCTCCACCAAGGGCCCATCGGCTTCCTCCCTCGCACACCTCTCCAGAGACACCTCG	400
Db	425	CAGCCTCCACCAAGGGCCCATCGGCTTCCTCCCTGGCAACCTCTCTCCAGAGACACCTCG	484
Qy	401	GGGGCACAGCGCCCTGGCTGCTTCAAGAGACTACTTCCCGGGAACCGGTGACGGTGT	460
Db	485	GGGGCACAGCGCCCTGGCTGCTTCAAGAGACTACTTCCCGGGAACCGGTGACCGTGT	544
Qy	461	CGTGGAACTCAGGCGCCCTGACACAGCGCGTGCACACTTCCTCCCGGTGTCTTACAGTCT	520
Db	545	CGTGGAACTCAGGCGCCCTGACACAGCGCGTGCACACTTCCTCCCGGTGTCTTACAGTCT	604
Qy	521	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCAGCAGCTTGGGCAACCCAGA	580
Db	605	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCAGCAGCTTGGGCAACCCAGA	664
Qy	581	CCTACATCTGCACGTTGAATCAAGCCACAGCAACACCAAGGTGGACAAGAAAGTGGAGC	640
Db	665	CCTACATCTGCACGTTGAATCAAGCCACAGCAACACCAAGGTGGACAAGAAAGTGGAGC	724
Qy	641	CCAAATCTTGTGACAAAACTCACACATCCCAACCGTGCCTCAGCAGCACTTGAAGTCCG	700
Db	725	CCAAATCTTGTGACAAAACTCACACATCCCAACCGTGCCTCAGCAGCACTTGAAGTCCG	784
Qy	701	CACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATCATCTCCCGGACCC	760
Db	785	GACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAGGACACCTCATCATCTCCCGGACCC	844
Qy	761	CTGAGGTACATCGCTGGTGGAGCTGAGCCAGAGACCCCTGAGGTCAAGTTCAACT	820
Db	845	CTGAGGTACATCGCTGGTGGAGCTGAGCCAGAGACCCCTGAGGTCAAGTTCAACT	904
Qy	821	GGTACGTGGAGCGCTGGAGGTGCATATGCCAAGACAAGCCGCGGAGGAGCAGTACA	880
Db	905	GGTACGTGGAGCGCTGGAGGTGCATATGCCAAGACAAGCCGCGGAGGAGCAGTACA	964
Qy	881	ACAGCAGTACCGCTGGTGGCTCAGCGTCTCACCGTCTGCACAGGACTTGGCTGAATGGCA	940
Db	965	ACAGCAGTACCGGGTGGCTCAGCGTCTCACCGTCTGCACAGGACTTGGCTGAATGGCA	1024
Qy	941	AGGAGTACAAAGTGCAGAGTCTCCACAAGCCCTCCAGCCCCCATCGAGAAACCACTCT	1000
Db	1025	AGGAGTACAAAGTGCAGAGTCTCCACAAGCCCTCCAGCCCCCATCGAGAAACCACTCT	1084
Qy	1001	CCAAAGCCAAAGGCGACGCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGGATG	1060
Db	1085	CCAAAGCCAAAGGCGACGCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGGATG	1144
Qy	1061	AGCTGACCAAGAACCAAGGTGTCCACAAGCCCTCCAGCCCCCATCGAGAAACCACTCT	1120
Db	1145	AGCTGACCAAGAACCAAGGTGTCCACAAGCCCTCCAGCCCCCATCGAGAAACCACTCT	1204
Qy	1121	TCGCGGTGGAGTGGGAGCAATGGGCGCGGAGAACAACTACAAGACCAACGCTCCCG	1180
Db	1205	TCGCGGTGGAGTGGGAGCAATGGGCGCGGAGAACAACTACAAGACCAACGCTCCCG	1264
Qy	1181	TGCTGGACTCCGACGGCTCTCTTCTCTAGCAAGACGCTACCGTGGACAAAGACGAGT	1240

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Db 1265 TGCTGGACTCCGAGCGCTCTTCTTCCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGT 1374
|||||
Qy 1241 GGCAGCAGGGGAACGCTTTCTTCTCATGCTCCGTCGATGCATGAGGCTCTGCACAACCACCTACA 1300
|||||
Db 1325 GGCAGCAGGGGAACGCTTTCTTCTCATGCTCCGTCGATGCATGAGGCTCTGCACAACCACCTACA 1384
|||||
Qy 1301 GCAGAGAGCCCTCTCCCTGTCTCCCGGTTAAATGA 1335
|||||
Db 1385 GCAGAGAGCCCTCTCCCTGTCTCCCGGTTAAATGA 1419
|||||

RESULT 8
US-10-066-895-27
; Sequence 27, Application US/10066895
; Patent No. US20020141990A1
; GENERAL INFORMATION:
; APPLICANT: Deen, Keith C.
;           Dillon, Susan B.
;           Porter, Terence C.
;           Sweet, Raymond A.
; TITLE OF INVENTION: Human Monoclonal Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19046
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/066,895
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/297,344
; FILING DATE: 1999-JUN-09
; APPLICATION NUMBER: 60/030,149
; FILING DATE: 01-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Geiger, Kathleen
; REGISTRATION NUMBER: 35,880
; REFERENCE/DOCKET NUMBER: P50504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5968
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-066-895-27

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Db 537 TCTGGGGCACAGCGCCCTGGCTGCTGTCAAGGACTACTTCCCGAACCGGTGACG 596
QY 457 GGTCTGTGAAGTCAAGGCGCTGACAGCGCGGTGCACACTTTCGCGGTGTCTACAG 516
Db 597 GTGTCTGTGAAGTCAAGGCGCTGACAGCGCGGTGCACACTTTCGCGGTGTCTACAG 656
QY 517 TCTCTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACC 576
Db 657 TCTCTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGACC 716
QY 577 CAGACTTACATCTGAAGTGAATCACAAGCCAGCAGCACAACAAAGGTGCACAAGAGTG 636
Db 717 CAGACTTACATCTGAAGTGAATCACAAGCCAGCAGCACAACAAAGGTGCACAAGAGTT 776
QY 637 GAGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGCAGCAGCTGAAGTCCG 696
Db 777 GAGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGCAGCAGCTGAAGTCCG 836
QY 697 GGGGACCTCAGTCTTCTCTTCCCGCCAAAACCCAGAGCACCCCTCATGATCTCCGG 756
Db 837 GGGGACCTCAGTCTTCTCTTCCCGCCAAAACCCAGAGCACCCCTCATGATCTCCGG 896
QY 757 ACCCTGAGTTCACATGCGTGTGTGACGTGAGCCAGCAGCAGCAGTCAAGTTC 816
Db 897 ACCCTGAGTTCACATGCGTGTGTGACGTGAGCCAGCAGCAGCAGTCAAGTTC 956
QY 817 AACTGTCAGTGGAGCGGTGAGTGCATATGCAAGACAAAGCCGCGGAGGAGCAG 876
Db 957 AACTGTCAGTGGAGCGGTGAGTGCATATGCAAGACAAAGCCGCGGAGGAGCAG 1016
QY 877 TACAACAGCAGTACCGTGTGTGTCAGCGTCTCACCGTCTCCAGCAGGACTGCTGAAT 936
Db 1017 TACAACAGCAGTACCGTGTGTGTCAGCGTCTCACCGTCTCCAGCAGGACTGCTGAAT 1076
QY 937 GCAAGGAGTACAAGTCAAGTCTCCAACAAAGCCCTCCAGCAGCAGCAGTCAAGAAAC 996
Db 1077 GCAAGGAGTACAAGTCAAGTCTCCAACAAAGCCCTCCAGCAGCAGCAGTCAAGAAAC 1136
QY 997 ATCTCCAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCGTCCCGCCATCCCG 1056
Db 1137 ATCTCCAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCGTCCCGCCATCCCG 1196
QY 1057 GATGAGTGCACAGAACCGTGTGAGCTGACCTGACCTGTGTCAGAGGCTTCTATCCAGC 1116
Db 1197 GAGGAGTGAACAGAACCGTGTGAGCTGACCTGACCTGTGTCAGAGGCTTCTATCCAGC 1256
QY 1117 GACATCGCGTGGAGTGGAGCAATGGGCGAGCGCGGAGACACTACAAGACACGCT 1176
Db 1257 GACATCGCGTGGAGTGGAGCAATGGGCGAGCGCGGAGACACTACAAGACACGCT 1316
QY 1177 CCGTGTCTGAGTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1236
Db 1317 CCGTGTCTGAGTCCGAGCGCTCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC 1376
QY 1237 AGTGGCAGCAGGGAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACAC 1296
Db 1377 AGTGGCAGCAGGGAAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACAC 1436
QY 1297 TACAGCAGAGAGGCTCTCCCTGCTCTCCGGGTAAATGA 1335
Db 1437 TACAGCAGAGAGGCTCTCCCTGCTCCCGGGTAAATGA 1475
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RESULT 11

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US-09-736-371B-20
; Sequence 20, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
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; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1347)
US-09-736-371B-20
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Query Match 85.0%; Score 1135; DB 10; Length 1347;
Best Local Similarity 91.4%; Pred. No. 1.4e-307;
Matches 1236; Conservative 0; Mismatches 90; Indels 27; Gaps 2;

QY 1 CAGGTGCAGCTGTGGAGTCTGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GAGGTCCAAGTGTGGAGTCTGGGCGGCTTTAGTCAGCCTGGAGGTCCTCTGAGACTC 60
QY 61 TCCTGTGCAGCTAGCGGATTTCATTTCAGTGGCTACTGGATGTCCTGGTCCGCCAGGCT 120
Db 61 TCCTGTGCAGCTTTCAGGATTTCATTTCAGTGGCTTTCCTAATGGCTGGGTCGCCAGGCT 120
QY 121 CCAGGGAAGGGCTCGAGTGGTGTGTAATTTAGATTGAAATCTGATATTTATGCAACA 180
Db 121 CCAGGGAAGGGCTCGAGTGGTGTGTAATTTAGATTGAAATCTGATATTTATGCAACA 180
QY 181 CATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 175 TACTATCGAGACTTCCGTGAGGCGGATTCATCTTCCAGAGATAATAGCAAAATACC 234
QY 241 CTCTATCTGCAATGAACGCCCTGAAACCGAGGACACAGCCGTGTTACTGTGTACA --- 297
Db 235 CTATACCTGCAATGAATAGTCTGAGGCTGAGGACACAGCCGTCTATTACTGTGCAAAA 294
QY 298 -----GATTTCTATAGACTGGGGCCAGGGAACACTAGTCAACCGTCTCC 339
Db 295 TTTTCGGCAGTACAGTGGTGGCTTTGATTAAGTGGGCGCAAGGGACCGTGTCTCC 354
QY 340 TCAGCCTCCACCAAGCGCCCATCGGCTTCCCGCTGGCACCCTCTCCCAAGAGCACCTCT 399
Db 355 TCAGCCTCCACCAAGCGCCCATCGGCTTCCCGCTGGCACCCTCTCCCAAGAGCACCTCT 414
QY 400 GGGGCGACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 459
Db 415 GGGGCGACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 474
QY 460 TCGTGAAGTCAAGCGCCCTGACCGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCC 519
Db 475 TCGTGAAGTCAAGCGCCCTGACCGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCC 534
QY 520 TCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCGTCCAGAGCTTGGGACCCAG 579
Db 535 TCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTCCCGTCCAGAGCTTGGGACCCAG 594
QY 580 ACCTACATCTGCAACGTGAATCACAAGCCAGCAGCACAACCAAGGTGCACAAGAGTGGAG 639
Db 595 ACCTACATCTGCAACGTGAATCACAAGCCAGCAGCACAACCAAGGTGCACAAGAGTGGAG 654
QY 640 CCCAAATCTGTGACAAAATCTCACATGCCACCGTCCCGCAGCAGCTGAATCTCGGGGG 699
Db 655 CCCAAATCTGTGACAAAATCTCACATGCCACCGTCCCGCAGCAGCTGAATCTCGGGGG 714
QY 700 GCACCGTCAAGTCTTCTCTTCCCGCAAAACCAAGGACACCTCTCATGATCTCCCGGACC 759
Db 715 GGACCGTCAAGTCTTCTCTTCCCGCAAAACCAAGGACACCTCTCATGATCTCCCGGACC 774
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Db 1136 GCGACATGCCCGTGGAGTGGGAGAGCAATGGGACGCCGAGAGCAACTACAGACCAGC 1195
QY 1175 CTCCTCGTGTGACTCCGACGCGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAGA 1234
Db 1196 CTCCTCGTGTGACTCCGACGCGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAGA 1255
QY 1235 GCAGGTGGCAGCAGGGAAGCTCTCTCATGCTCGTGATCATGAGGCTCTGCACACAC 1294
Db 1256 GCAGGTGGCAGCAGGGAAGCTCTCTCATGCTCGTGATGATGAGGCTCTGCACACAC 1315
QY 1295 ACTACACGAGAAGAGCCT 1335
Db 1316 ACTACACGAGAAGAGCCT 1356

RESULT 13

US-10-066-895-14

; Sequence 14, Application US/10066895

; Patent No. US20020141990A1

; GENERAL INFORMATION:

; APPLICANT:

; Dillion, Susan B.

; Porter, Terence C.

; Sweet, Raymond A.

; TITLE OF INVENTION: Human Monoclonal Antibodies

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19046

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/066,895

; FILING DATE: 04-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/297,344

; FILING DATE: 1999-JUN-09

; APPLICATION NUMBER: 60/030,149

; FILING DATE: 01-NOV-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Geiger, Kathleen

; REGISTRATION NUMBER: 35,880

; REFERENCE/DOCKET NUMBER: P50504

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5968

; TELEFAX: 610-270-5090

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6284 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-066-895-14

Query Match 84.6%; Score 1128.8; DB 12; Length 6284;
Best Local Similarity 91.2%; Pred. No. 1.2e-305;
Matches 1231; Conservative 0; Mismatches 92; Indels 27; Gaps 2;

QY 7 CAGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCTCTGT 66
Db 1081 CTGCTCAGGAGTCTGGGGGAGGCTGTGTCAGGCTGGCGGTCCCTTAAGACTCTCTGT 1140

QY 67 GCAGCTAGCGGATTACATTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTCCAGGG 126
Db 1141 GCAGCCTCTTGGAAACACCCCTCAGTGGCTATACCATGCTGCTGGGTCCGCCAGGCTCCAGGG 1200
QY 127 AAGGGCTCGAGTGGGTGCTGAAATTTAGATTTGAAATTTGATATTTATATGCAACACATTTAT 186
Db 1201 AAGGGCTCGAGTGGGTGCTCATCAATTT-----ACTGGAGGTAGCAACTTCATAAACTAC 1254
QY 187 GCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGACTGTAT 246
Db 1255 TCAGACTCAGTGAAGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCTACTTTAT 1314
QY 247 CTGCAATGAACAGCCTGAAACCGAGGACACAGCGTGTATTTACTGT----- 294
Db 1315 CTGCAATGAACAGCCTGACAGCCGAGGACACGGCTGTCTATTATTGTGTGGACCGCCCT 1374
QY 295 -----ACAGATTTTCATAGACTGGGGCCAGGGAACACTAGTCAACCGTCTCTCAGCC 345
Db 1375 ATAGCACCGCCTACTTTTGACCACTGGGGCCAGGGAACCTGTCTACCGTCTCTCAGCC 1434
QY 346 TCCACCAAGGGCCCATCGGTCTTCCCGCTGGGACCCCTCTCCAAAGAGACCTCTGGGGGC 405
Db 1435 TCCACCAAGGGCCCATCGGTCTTCCCGCTGGGACCCCTCTCCAAAGAGACCTCTGGGGGC 1494
QY 406 ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGTCTGG 465
Db 1495 ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGTCTGG 1554
QY 466 AACTCAGGCGCTGACCGGCGTGCACACCTTCCCGGCTGTCTACAGCTCTCAGGA 525
Db 1555 AACTCAGGCGCTGACCGGCGTGCACACCTTCCCGGCTGTCTACAGCTCTCAGGA 1614
QY 526 CTCTACTCTCCTCAGCAGCGTGGTACCGTGGCCCTCAGCAGCTTGGGACCCAGACCTAC 585
Db 1615 CTCTACTCTCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1674
QY 586 ATCTGCAAGTGAATCACAAGCCAGCAGCAACACCAAGGTGGACAAGAAAGTGGAGCCAAA 645
Db 1675 ATCTGCAAGTGAATCACAAGCCAGCAGCAACACCAAGGTGGACAAGAAAGTGGAGCCAAA 1734
QY 646 TCTTGTGACAAAAGTCAACATGCCCGTGGCCAGCAGCTGAACTCGCGGGGACCG 705
Db 1735 TCTTGTGACAAAAGTCAACATGCCCGTGGCCAGCAGCTGAACTCGCGGGGACCG 1794
QY 706 TCAGTCTTCTCTTCCCGCCAAACCAAGACACCTCATGCTCCTCCCGGACCCCTGAG 765
Db 1795 TCAGTCTTCTCTTCCCGCCAAACCAAGACACCTCATGCTCCTCCCGGACCCCTGAG 1854
QY 766 GTCACATGCTGTGGTGGACGTGAGCCACGAGACCTCTGAGGTCAAGTTCAACTGGTAC 825
Db 1855 GTACATGCTGTGGTGGACGTGAGCCACGAGACCTCTGAGGTCAAGTTCAACTGGTAC 1914
QY 826 GTGGACGGCGTGGAGTGTATATGCCAGACAAGCCCGGGGAGGAGCAGTACACAGC 885
Db 1915 GTGGACGGCGTGGAGTGTATATGCCAGACAAGCCCGGGGAGGAGCAGTACACAGC 1974
QY 886 AGTACCGTGTGTGTGAGCGTCTCTCAGCGTCTGACCGAGCTGGCTGAATGGCAAGGAG 945
Db 1975 AGTACCGGCTGTGAGCGTCTCTCAGCGTCTGACCGTCTGACCGAGGAGTGGCTGATGGCAAGGAG 2034
QY 946 TACAAGTGAAGTCTTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAACCATCTCCAAA 1005
Db 2035 TACAAGTGAAGTCTTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAACCATCTCCAAA 2094
QY 1006 GCCAAGGCGCAGCCCGGAGAACACAGGTGTACACCTTCCCGCCCATCCCGGATGAGTGTG 1065
Db 2095 GCCAAGGCGCAGCCCGGAGAACACAGGTGTACACCTTCCCGCCCATCCCGGATGAGTGTG 2154
QY 1066 ACCAAGAACAGGTGTGAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGGACATGCC 1125
Db 2155 ACCAAGAACAGGTGTGAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGGACATGCC 2214
QY 1126 GTGGAGTGGGAGCAATGGGCGAGCGGAGAACTACAAGAACACGCTCCCGTGTGTG 1185

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 55.2959 Seconds
(without alignments)
7404.053 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1147.2	85.9	1437	3	US-08-487-550-7
2	1143.6	85.7	1576	1	US-08-157-101A-6
3	1141.2	85.5	19040	4	US-09-343-485A-3
4	1140.6	85.4	1350	1	US-08-157-101A-9
5	1082.6	81.1	8120	3	US-09-027-449-68
6	1082.6	81.1	8120	3	US-09-026-985-68
7	1082.6	81.1	8120	4	US-09-121-952A-68
8	1082.6	81.1	8120	4	US-09-234-340A-68
9	1066.4	79.9	1655	3	US-09-049-672A-21
10	1063.4	79.7	6557	1	US-08-286-740-3
11	1063.4	79.7	6557	5	PCT-US93-09576-3
12	1042.6	78.1	1617	2	US-08-378-939-9
13	1040.6	77.9	1431	3	US-08-487-550-11
14	1039.8	77.9	1418	4	US-08-793-450-7
15	1039.8	77.9	9209	1	US-08-149-099C-3
16	1039.8	77.9	9209	1	US-08-476-275-2
17	1039.8	77.9	9209	2	US-08-478-567A-3
18	1039.8	77.9	9209	4	US-08-475-815B-3
19	1039.8	77.9	18986	2	US-08-819-866-2
20	1039.8	77.9	18986	2	US-09-023-715-2
21	1039.8	77.9	18986	4	US-09-343-485A-2
22	1039	77.8	1567	3	US-09-049-672A-17
23	1035	77.5	1329	5	PCT-US96-13152-3
24	1021.4	76.5	1431	3	US-08-487-550-3
25	1020.6	76.4	1404	4	US-09-485-737B-66
26	1020.6	76.4	2133	4	US-09-485-737B-89
27	1018.6	76.3	1428	1	US-08-488-376-19

28	1018.6	76.3	1428	2	US-08-634-223-19	Sequence 19, Appl
29	1018.6	76.3	1428	2	US-08-634-224-19	Sequence 19, Appl
30	1018.6	76.3	1428	2	US-08-634-400-19	Sequence 19, Appl
31	1018.6	76.3	1428	2	US-08-635-878-19	Sequence 19, Appl
32	1018.6	76.3	1428	2	US-08-770-057-19	Sequence 19, Appl
33	1018.6	76.3	1428	4	US-09-335-697B-19	Sequence 19, Appl
34	1018.6	76.3	1428	4	US-09-335-697B-19	Sequence 19, Appl
35	1017	76.2	1428	1	US-08-488-376-17	Sequence 17, Appl
36	1017	76.2	1428	2	US-08-634-223-17	Sequence 17, Appl
37	1017	76.2	1428	2	US-08-634-224-17	Sequence 17, Appl
38	1017	76.2	1428	2	US-08-634-400-17	Sequence 17, Appl
39	1017	76.2	1428	2	US-08-635-878-17	Sequence 17, Appl
40	1017	76.2	1428	2	US-08-770-057-17	Sequence 17, Appl
41	1017	76.2	1428	4	US-09-335-697B-17	Sequence 17, Appl
42	1017	76.2	1428	4	US-09-335-697B-17	Sequence 17, Appl
43	1011	75.7	1135	1	US-08-236-311-8	Sequence 8, Appl
44	1011	75.7	1135	3	US-08-457-918-8	Sequence 8, Appl
45	1000	74.9	6285	1	US-08-467-420A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-487-550-7
; Sequence 7, Application US/08487550
; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1437 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1437

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 1..1437

US-08-487-550-7

Query Match 85.9%; Score 1147.2; DB 3; Length 1437;

Best Local Similarity 90.7%; Pred. No. 6, 2e-264;									
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;									
QY	1	GAGTGTGAGTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC	60						
Db	58	GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCAGCCTCGCGGGTCCCTTGAGAGTC	117						
QY	61	TCCTGTGACGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT	120						
Db	118	TCCTGTGACGCTCTGGAATTCACCTTCAGTGACCACTACATGATTTGGTTCCGCCAGGCT	177						
QY	121	CCAGGGAAGGGGCTCGAGTGGTGGTGAATTTAGATTGAATCTGATAATTTATGCAACA	180						
Db	178	CCAGGGAAGGGGCGGAATGGTAGGTTTCATTAGAAACAACCGAAGCGTGGGACAACA	237						
QY	181	CATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAGAGATGATTCAAATCTAGA	240						
Db	238	GAATACCGCGCTGTGTGAAGACAGATTCACCATCTCCAGAGATGATTCAAAGCATC	297						
QY	241	CTGTATCTGCAAAATGAACAGCCTGAAACCGAGCACACGCCGTGTATTACTGTAC----	296						
Db	298	GCCTATCTGCAATGACGACGCTGAAATCGAGGACACGCCGTCTATTACTGTACTACA	357						
QY	297	-----AGATTTCATAGACTGGGGC	315						
Db	358	TCCTACATTTTCACATTTCTCGGGGTGGTGTCTGTATGGAGGTTACTTCGAATTTCTGGGC	417						
QY	316	CAGGGAACACTAGTTCACGGTCTCTCAGCTCCACCAAGGGCCCATCGGTCCTCCCGCTG	375						
Db	418	CAGGGCGCCCTGGTTCACCGTCTCTCAGCTAGCACCAAGGGCCCATCGGTCCTCCCGCTG	477						
QY	376	GCACCTCTCTCCAAAGAGCACCTCTGGGGGACACAGCGCCCTGGGTCCTCGGTCAAGGAC	435						
Db	478	GCACCTCTCTCCAAAGAGCACCTCTGGGGGACACAGCGCCCTGGGTCCTCGGTCAAGGAC	537						
QY	436	TACTTCCCGAACCGGTGACGGTGTGTGNACTCAGGCGCCCTGACAGCGGGGCTGCAC	495						
Db	538	TACTTCCCGAACCGGTGACGGTGTGTGNACTCAGGCGCCCTGACAGCGGGGCTGCAC	597						
QY	496	ACCTTCCCGGTGCTTACAGTCTCTCAGGACTTACTTCCCTCAGCAGCGGTGGTGAACG	555						
Db	598	ACCTTCCCGGTGCTTACAGTCTCTCAGGACTTACTTCCCTCAGCAGCGGTGGTGAACG	657						
QY	556	CCCTCCAGCAGCTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAAC	615						
Db	658	CCCTCCAGCAGCTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAAC	717						
QY	616	ACCAAGTGGACAAGAAAGTGGAGCCCAAAATCTTGTGACAAAACCTCACATGCCACCG	675						
Db	718	ACCAAGTGGACAAGAAAGTGGAGCCCAAAATCTTGTGACAAAACCTCACATGCCACCG	777						
QY	676	TGCCCAGCACCTGAACCTCGCGGGGACCGCTGACGTCTTCTTCCCGCCCAAAACCCAAAG	735						
Db	778	TGCCCAGCACCTGAACCTCGCGGGGACCGCTGACGTCTTCTTCCCGCCCAAAACCCAAAG	837						
QY	736	GACACCTCATGATCTCCGGNACCCTCAGCTCAGCTCAGTGGTGGAGCTGAGCCAC	795						
Db	838	GACACCTCATGATCTCCGGNACCCTCAGCTCAGCTCAGTGGTGGAGCTGAGCCAC	897						
QY	796	GAAGACCTGTAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG	855						
Db	898	GAAGACCTGTAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG	957						
QY	856	ACAAAGCCCGGGAGGAGCAGTACAAACAGCAGGTACCGTGTGGTCCCTCACCGTC	915						
Db	958	ACAAAGCCCGGGAGGAGCAGTACAAACAGCAGGTACCGTGTGGTCCCTCACCGTC	1017						
QY	916	CTGCACCGAGTCTGCTGAATGGCAGGAGTACAAGTCTCAAGGCTCTCAACAAAGCCCTC	975						
Db	1018	CTGCACCGAGTCTGCTGAATGGCAGGAGTACAAGTCTCAAGGCTCTCAACAAAGCCCTC	1077						
QY	976	CCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCAAGGTG	1035						

Db	1078	CCAGCCCCCATGAGAAACCACTCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTG	1137
QY	1036	TACACCTTGCCTCCATCCGGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGACCTG	1095
Db	1138	TACACCTTGCCTCCATCCGGGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGACCTG	1197
QY	1096	GTCAAAGGCTTCTATCCAGCGGACATCCCGTGGAGTGGGAGAGCAATGGGAGCCGAG	1155
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QY	1156	ACAACACTCAAGACACACCGCTCCCGTGGACTCCGAGCGGCTCTTCTCTCTACAGC	1215
Db	1258	ACAACACTCAAGACACACCGCTCCCGTGGACTCCGAGCGGCTCTTCTCTCTACAGC	1317
QY	1216	AAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGAGGAACTTCTCTCATGTCCGTGATG	1275
Db	1318	AAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGAGGAACTTCTCTCATGTCCGTGATG	1377
QY	1276	CATGAGGCTCTGCACCAACCACTACAGCAGAGAGACCTCTCCCTGTCTCCGGGTAAATGA	1335
Db	1378	CATGAGGCTCTGCACCAACCACTACAGCAGAGAGACCTCTCCCTGTCTCCGGGTAAATGA	1437

RESULT 2

US-08-157-101A-6
; Sequence 6, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-6

Query Match 85.7%; Score 1143.6; DB 1; Length 1576;
Best Local Similarity 91.6%; Pred. No. 4, 6e-263;
Matches 1244; Conservative 0; Mismatches 84; Indels 30; Gaps 2;

Qy	2	AGTGCAGCTGGTGGAGCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACACTCT	61
Db	43	AGSTGCAGCTGGTGGAGCTTGGGGGAGGGCTGCTCCAGCCTGGGAGTCCCTTGACACTCT	102
Qy	62	CCTGTGCAGCTAGCGGATTCACCTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC	121
Db	103	CCTGTGCAGCCTTGGATTTCACCTTCAGTAGCAATTCTATGCACGTGGGTCCGCCAGGCTC	162
Qy	122	CAGGGAAGGGCTCGATGGGTTCTCGAAATTAGATTGAAATCTGATAATTATCAACAC	181
Db	163	CAGCAAGGGGTTGGAGTGGGTGGCAGTTA-----TATTATATGATGAAATCATAAAT	216
Qy	182	ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAGAGATGATTTCAAAATCTAGAC	241
Db	217	TCTACGCAGACTCCGTGAAGGGCGGATTCACCATTTCCAGAGCAATTTCCAAGAACAAC	276
Qy	242	TGTATCTGCAANTGAACAGCCTGAAACCGAGSACACAGCCGTGTATTACTGTACA----	297
Db	277	TGTATCTGGAAGTGAAGAGCCTGCAAACTGAGSACAGGGTGTCTATTACTGTATAAGAG	336
Qy	298	-----GATTTTCATAGACTGGGGCCAGGGAACACTAGTTCACCGTCT	337
Db	337	ATCAAACTTACGGAGTCCACAGATTTCATCTCTGGGGCCAGGAAACCTTGCTCAGCGTCT	396
Qy	338	CCTCAGCCTCCACAAAGGGCCATCGGCTCTCCCTCGACCCCTCTCTCAAGAGCACT	397
Db	397	CCTCAGCCTCCACAAAGGGCCATCGGCTCTCCCTCGACCCCTCTCTCAAGAGCACT	456
Qy	398	CTGGGGCACAGGGCCCTGGGCTGGCTGGTCAAGACTACTTCCCGAACCGGTGACGG	457
Db	457	CTGGGGGCACAGGGCCCTGGGCTGGTCAAGACTACTTCCCGAACCGGTGACGG	516
Qy	458	TGTCGTGGAACTCAGCGGCCCTGACCAGGGGGTGACACCTTCCCGGCTCTCTACAGT	517
Db	517	TGTCGTGGAACCTCAGCGGCCCTGGCCAGCGGGTGCACACTTCCCGGCTCTCTACAGT	576
Qy	518	CCTCAGACTCTACTCCCTCAGAGCGGTGGTGACCGTGCCCTCCAGSAGCTTGGGCACCC	577
Db	577	CCTCAGACTCTACTCCCTCAGAGCGGTGGTGACCGTGCCCTCCAGSAGCTTGGGCACCC	636
Qy	578	AGACCTACATCTCAAGTGAATCAACAGCCAGCAACCAAGGTGACAAAGAAAGTG	637
Db	637	AGACCTACATCTCAAGTGAATCAACAGCCAGCAACCAAGGTGACAAAGAAAGTG	696
Qy	638	AGCCCAATCTTGTGCAAACTCACATGCCACCGTGCCCGCCAGSAGCTGAATCTCGG	697
Db	697	AGCCCAATCTTGTGCAAACTCACATGCCACCGTGCCCGCCAGSAGCTGAATCTCGG	756
Qy	698	GGCACCGTCAGCTTCCTTTCCCCCAAAACCCAGGACACCGCTATGATCTCCCGGA	757
Db	757	GGGACCGTCAGCTTCCTTTCCCCCAAAACCCAGGACACCGCTATGATCTCCCGGA	816
Qy	758	CCCTCAGGTACATCGTGGTGGAGCGTGAGCCAGGAAGACCTGAGGTCAAGTTCA	817
Db	817	CCCTCAGGTACATCGTGGTGGAGCGTGAGCCAGGAAGACCTGAGGTCAAGTTCA	876
Qy	818	ACTGGTACTGGACGCGGTGGAGGTGCATATGCCACAGAAAGCCGGGAGGAGCAGT	877
Db	877	ACTGGTACTGGACGCGGTGGAGGTGCATATGCCACAGAAAGCCGGGAGGAGCAGT	936
Qy	878	ACAACAGCACGTACCGTGGTGGTGGAGCGTCCACCGTCTGCACAGGACTGGCTGAATG	937
Db	937	ACAACAGCACGTACCGGTTGGTTCAGGTCCTCACGTCCTGCACAGGACTGGCTGAATG	996
Qy	938	GCNAGAGTACAGTGCAGGTTCTCCACAAAGCCCTCCCGAGCCCCCATCGAGAAACCA	997
Db	997	GCNAGAGTACAGTGCAGGTTCTCCACAAAGCCCTCCCGAGCCCCCATCGAGAAACCA	1056
Qy	998	TCTCCAAAGCCAAAGGACGCCCGAGAACCAAGGTGTACACCTGCCCCATCCCGG	1057
Db	1057	TCTCCAAAGCCAAAGGACGCCCGAGAACCAAGGTGTACACCTGCCCCATCCCGG	1116
Qy	1058	ATGAGTGTACCAGAAACAGGTGACCTTGCTGGTCAAAAGGTTCTATCCCAAGC	1117

Db	1117	ATGAGCTGACCAAGACCAGGTGAGCCTGACCTGCGCTGGTCAAGAGCTTCTATCCACGG	1176
Qy	1118	ACATCGCGGTGGAGTGGGAGAGCAATGGCGACGCGGAGAACAACTACAAGACCAACGCCTC	1177
Db	1177	ACATCGCGGTGGAGTGGGAGAGCAATGGCGACGCGGAGAACAACTACAAGACCAACGCCTC	1236
Qy	1178	CCGTGCTGGACTCCGACGGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGACA	1237
Db	1237	CCGTGCTGGACTCCGACGGGCTCCTTCTCTACAGCAAGCTCACCGTGGACAAAGACA	1296
Qy	1238	GTCGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGATGAGGCTCTGCACAACCACT	1297
Db	1297	GTCGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGATGAGGCTCTGCACAACCACT	1356
Qy	1298	ACAGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1335
Db	1357	ACAGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1394

RESULT 3

```

US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 641377
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

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Query Match 85.5%; Score 1141.2; DB 4; Length 19040;
Best Local Similarity 92.0%; Pred. No. 3.6e-262;
Matches 1246; Conservative 0; Mismatches 83; Indels 25; Gaps 3;

Query Match 85.5%; Score 1141.2; DB 4; Length 19040;
Best Local Similarity 92.0%; Pred. No. 3.6e-262;
Matches 1246; Conservative 0; Mismatches 83; Indels 25; Gaps

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QY 295 AC-----AGATTTCATAGACTGGGCGCAGGAAACACTAGTCACCGTCTCCTC 341
Db 9787 CGAGCTTGACTACAGGCTCTGACTCCCTGGGCGCAGGAGTCTCTGTCACCGTCTCCTC 9846
QY 342 AGGCTCCCAAGGGCCATCGGCTTCCCGCTGGGACCGCTCTCCAGAGCACCTCTGG 401
Db 9847 AGCTAGCACCAAGGGCCATCGGCTTCCCGCTGGGACCGCTCTCCAGAGCACCTCTGG 9906
QY 402 GGGCAGACGGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGC 461
Db 9907 GGGCAGACGGGCGCTGGCTGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGC 9966
QY 462 GTGGAACCTCAGGGCGGCTGACCGAGCGGCTGCACACCTTCCCGGCTGTCTTACAGTCTC 521
Db 9967 GTGGAACCTCAGGGCGGCTGACCGAGCGGCTGCACACCTTCCCGGCTGTCTTACAGTCTC 10026
QY 522 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGCGCTTCCAGCAGCTTGGGCACCCAGAC 581
Db 10027 AGGACTCTACTCCCTCAGCAGCGTGTGACCGTGTGCGCTTCCAGCAGCTTGGGCACCCAGAC 10086
QY 582 CTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCC 641
Db 10087 CTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCC 10146
QY 642 CAAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCGCGGGGGC 701
Db 10147 CAAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCGCGGGGG 10206
QY 702 ACCGTGAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 761
Db 10207 ACCGTGAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 10266
QY 762 TGAGGTCAATCGCTGGTGTGGAGCTGAGCCAGCAAGAGCCCTGAGTCAAGTTCAACTG 821
Db 10267 TGAGGTCAATCGCTGGTGTGGAGCTGAGCCAGCAAGAGCCCTGAGTCAAGTTCAACTG 10326
QY 822 GTAGCTGGAGCGGCTGAGGTGCAATATGCCAAGACAAAGCCGCGGAGAGCAGTACAA 881
Db 10327 GTAGCTGGAGCGGCTGAGGTGCAATATGCCAAGACAAAGCCGCGGAGAGCAGTACAA 10386
QY 882 CAGCAGGTACCGTGTGGTGCAGCGTCTCAGCGTCTCCAGCAGGACTGCGTGAATGGCAA 941
Db 10387 CAGCAGGTACCGTGTGGTGCAGCGTCTCAGCGTCTCCAGCAGGACTGCGTGAATGGCAA 10446
QY 942 GGAGTACAAGTGCAGGTCTTCAACAAGCCCTCCAGCCCGCCATCGAGAAACCATCTC 1001
Db 10447 GGAGTACAAGTGCAGGTCTTCAACAAGCCCTCCAGCCCGCCATCGAGAAACCATCTC 10506
QY 1002 CAAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGA 1061
Db 10507 CAAAGCCAAAGGCGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGA 10566
QY 1062 GCTGACCAAGAACAGGTGCAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACAT 1121
Db 10567 GCTGACCAAGAACAGGTGCAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACAT 10626
QY 1122 CGCGGTGGAGTGGGAGAGCAATGGGAGCGGAGGAGAACAACTACAAGACACCGCTCCCGT 1181
Db 10627 CGCGGTGGAGTGGGAGAGCAATGGGAGCGGAGGAGAACAACTACAAGACACCGCTCCCGT 10686
QY 1182 GCTGAGCTCCAGCGGCTCTTCTTCTCTCAGCAAGCTCAGCGTGCAGAGACAGGTG 1241
Db 10687 GCTGAGCTCCAGCGGCTCTTCTTCTCTCAGCAAGCTCAGCGTGCAGAGACAGGTG 10746
QY 1242 GCAGCAGGGGAGCGTCTTCTCTCATGCTCGTGTATGATGAGCTGTGCAACACCACTACAC 1301
Db 10747 GCAGCAGGGGAGCGTCTTCTCTCATGCTCGTGTATGATGAGCTGTGCAACACCACTACAC 10806
QY 1302 GCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 10807 GCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 10840
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RESULT 4
US-08-157-101A-9
; Sequence 9, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGERAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-9
Query Match 85.4%; Score 1140.6; DB 1; Length 1350;
Best Local Similarity 91.6%; Pred. No. 2.3e-262;
Matches 1241; Conservative 0; Mismatches 84; Indels 30; Gaps 2;
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QY 2 AGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGTCCTTACACTCT 61
Db 2 AGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGAGGTCCTTGAGACTCT 61
QY 62 CTTGTGCAGCTACGGGATTCACCTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 121
Db 62 CTTGTGCAGCTTGGATTCACCTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 121
QY 122 CAGGGAAGGGCTCGAGTGGTGGTGGTGAATTTAGATTGAATCTGATAATTTATGCAACAC 181
Db 122 CAGGGAAGGGTGGAGTGGTGGCAGTTA-----TATTATATGATGGAATCATAAT 175
QY 182 ATTATCGGAGTCTGGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 176 TCTACCGACACTCCGTTGAAGGGCCGATTCACCATTTCCAGAGACAAATTCAGAGACACAC 235
QY 242 TGTATCTGCAAAATCAACAGCCTCAAAACCCGAGACACACAGCCGTGTATTACTACTACA---- 297
Db 236 TGTATCTGGAAGTGAAGAGCCTGCAAACTGAGACACAGGCTGTCTATTACTGTATAAGAG 295
QY 298 -----GATTTTCATAGCTGGGGCCAGGGAACACACTAGTCAACCGTCT 337
Db 296 ATCAAACTACGGAGTCCACAGATTTTGACTCTCTGGGGCCAGGGAACCCCTGGTCAACCGTCT 355
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QY 451 GTGACGGTGTCTGTGAACCTCAGGGCCCTGACACGCGGTGCACACTTCCCGGCTGTC 510
Db 1837 GTGACGGTGTCTGTGAACCTCAGGGCCCTGACACGCGGTGCACACTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCAGCAGCTTG 570
Db 1897 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCAGCAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGAAGTGAATCACAAGCCAGCACACACAGGTTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGAAGTGAATCACAAGCCAGCACACACAGGTTGGACAAG 2016
QY 631 AAGTGGAGCCCAACTTGTGACAAACTCACAACATGCCACCGTGCCTCAGCAGCTGAA 690
Db 2017 AAGTGGAGCCCAACTTGTGACAAACTCACAACATGCCACCGTGCCTCAGCAGCTGAA 2076
QY 691 CTCGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCAAGACACCTCATGATC 750
Db 2077 CTCCTGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCAAGACACCTCATGATC 2136
QY 751 TCCGGGACCCCTGAGGTACATCTGCTGTGACGTGAGCCAGAACCCCTGAGGTC 810
Db 2137 TCCGGGACCCCTGAGGTACATCTGCTGTGACGTGAGCCAGAACCCCTGAGGTC 2196
QY 811 AAGTTCAACTGTTAGTGGAGCGGTGAGGTGCATATGCCAAGACAAAGCCGCGGAG 870
Db 2197 AAGTTCAACTGTTAGTGGAGCGGTGAGGTGCATATGCCAAGACAAAGCCGCGGAG 2256
QY 871 GAGCAGTACACACGACGTACCGTGTGTCAGCTCTCACCCTGTCACACGAGTGG 930
Db 2257 GAGCAGTACACACGACGTACCGTGTGTCAGCTCTCACCCTGTCACACGAGTGG 2316
QY 931 CTGAATGCAAGGAGTACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCATCGAG 990
Db 2317 CTGAATGCAAGGAGTACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCATCGAG 2376
QY 991 AAACCATCTCCAAGCAAGGACGCGCCGAGAGCAATGGGAGCAATGGGAGCAACTACAAGAC 1050
Db 2377 AAACCATCTCCAAGCAAGGACGCGCCGAGAGCAATGGGAGCAACTACAAGAC 2436
QY 1051 TCCCGGATGATGATGACCAAGAACGAGTCAAGCTGACCTGACCTGGTCAAGGCTTCTAT 1110
Db 2437 TCCCGGAGAGATGACCAAGAACGAGTCAAGCTGACCTGACCTGGTCAAGGCTTCTAT 2496
QY 1111 CCCAGCAGATCCGCGTGGAGTGGAGAGCAATGGGAGCCGAGCAACTACAAGAC 1170
Db 2497 CCCAGCAGATCCGCGTGGAGTGGAGAGCAATGGGAGCCGAGCAACTACAAGAC 2556
QY 1171 ACGCTCCCGTGTGGACTCCGAGGCTCCTCTCTCTACAGCAAGCTCACCGTGGAC 1230
Db 2557 ACGCTCCCGTGTGGACTCCGAGGCTCCTCTCTCTACAGCAAGCTCACCGTGGAC 2616
QY 1231 AAGAGAGGTGGCAGCAGGGAAGCTCTCTCTATGCTTCCGTGATGATGAGGCTCTGCAC 1290
Db 2617 AAGAGAGGTGGCAGCAGGGAAGCTCTCTCTATGCTTCCGTGATGATGAGGCTCTGCAC 2676
QY 1291 AACCACTACAGCAGAGAGCCCTCTCCTGTCTCCGGTAAATGA 1335
Db 2677 AACCACTACAGCAGAGAGCCCTCTCCTGTCTCCGGTAAATGA 2721
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RESULT 7

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US-09-121-952A-68
; Sequence 68, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrrok, Zahra
; APPLICANT: Zapata, Gerardo A.
```

```
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8120 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-121-952A-68
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Query Match

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Best Local Similarity 81.1%; Score 1082.6; DB 4; Length 8120;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;
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QY 1 GAGGTGCAGCTGTGTGGAGGCTGTGGGAGGCTTGGTAAAGCCGCGGGTCCCTTAGACTC 60
Db 1363 GAAGTTCACCTAGTCGAGTCTGGCGTGGCTGGTGCAGCCAGGGGCTCATCTCGTTG 1422
QY 61 TCTGTGACGTAGCGGATTCACCTTCACTGGCTACTGGATGTCCTGGGTCCGCGAGCT 120
Db 1423 TCTGTGACGTACTGGTACTCTCTCGAGTCACTATATGCTGCTGGTCCGTGAGGC 1482
QY 121 CCAGGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTGATAATATCAACA 180
Db 1483 CCGGTGAAGGCTCGAATGGTTGATATTT-----GATCCTTCCAAATGGTGAAC 1536
QY 181 CATTTGCGGAGTCTGTGAAGGGGAAATTCACCTCTCAAGAGATGATCAAAATCTAGA 240
Db 1537 ACGTATAATCAAAAGTTCAGGGCGCTTTCACCTTTATCTCGGACAACTCCAAAACACA 1596
QY 241 CTGTATCTCAAAATCAACAGCCTGAAACCCAGGACAGCGGTGTATTTACTGTACA --- 297
Db 1597 GCATACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCGGTCTATTTACTGTGCAAGA 1656
QY 298 -----GATTTCAATAGACTGGGCGCAGGACACTAGTC 330
Db 1657 GGGGATTATCGTACAAATGGTGACTGTTCTTCGACGCTCTGGGGTCAAGGAACCTGGTC 1716
QY 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCTCAAG 390
Db 1717 ACCGTCTCTCTCGGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCTCAAG 1776
QY 391 AGCACTCTGGGGGACAGCGGCCCTGGGCTGCTTGGTCAAGGACTACTTCCCCGAACCG 450
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Db 1717 ACCGTCCTCGGCTCCACCAAGGGCCCTCGTCTTCCCTCGGACCCCTCTCAAG 1776
QY 391 AGCACCCTCTGGGGGACAGCGGCGCTGGCTGCTCTGAAGACTACTTCCCGCAACCG 450
Db 1777 AGCACCCTCTGGGGGACAGCGGCGCTGGCTGCTCTGAAGACTACTTCCCGCAACCG 1836
QY 451 GTGCGGCTCTGTGAACCTCAGGGGCGCTGACACAGCGCGCTGACACCTTCCCGGCTGTC 510
Db 1837 GTGCGGCTCTGTGAACCTCAGGGGCGCTGACACAGCGCGCTGACACCTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCAGGACTACTTCCCTAGCAGCGTGTGACCGTGCCTCCACAGCTTG 570
Db 1897 CTACAGTCTCAGGACTACTTCCCTAGCAGCGTGTGACCGTGCCTCCACAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGCAAGTGAATCACAAGCCCAAGACACCAAGGTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGCAAGTGAATCACAAGCCCAAGACACCAAGGTGGACAAG 2016
QY 631 AAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACTGAA 690
Db 2017 AAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACTGAA 2076
QY 691 CTCGCGGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCCCAAGGACACCCCTCATGATC 750
Db 2077 CTCCTGGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCCCAAGGACACCCCTCATGATC 2136
QY 751 TCCCGGACCCCTGAGGTACATGCGTGTGTGACGTGAGCCAGCAAGACCTTGAGTGC 810
Db 2137 TCCCGGACCCCTGAGGTACATGCGTGTGTGACGTGAGCCAGCAAGACCTTGAGTGC 2196
QY 811 AAGTTCAACTGTAGCTGAGCGGTGAGGTGCATATGCAAGACCAAGACCGCGGGAG 870
Db 2197 AAGTTCAACTGTAGCTGAGCGGTGAGGTGCATATGCAAGACCAAGACCGCGGGAG 2256
QY 871 GAGCAGTACACAGCAGCTACCGTGTGTGAGCTGCTTACCGTCTGTCACAGGACTGG 930
Db 2257 GAGCAGTACACAGCAGCTACCGTGTGTGAGCTGCTTACCGTCTGTCACAGGACTGG 2316
QY 931 CTGAATGGCAAGGACTACAAGTGCAGGTCTCCAAAGACCCCTCCAGCGCCCATCGAG 990
Db 2317 CTGAATGGCAAGGACTACAAGTGCAGGTCTCCAAAGACCCCTCCAGCGCCCATCGAG 2376
QY 991 AAAACCATCTCCAAAGCCAAAGGGCAGCGCCGAGAACACAGGTGTACACCTGCCGCCA 1050
Db 2377 AAAACCATCTCCAAAGCCAAAGGGCAGCGCCGAGAACACAGGTGTACACCTGCCGCCA 2436
QY 1051 TCCCGGGATGAGTGCACCAAGAACAGCTCAGCTGACCTGCCTGGTCAAGGCTTCTAT 1110
Db 2437 TCCCGGGAGAGATGACCAAGAACAGCTGAGCTGACCTGCCTGGTCAAGGCTTCTAT 2496
QY 1111 CCCAGGACATCGCGTGGAGTGGAGAGCAANTGGCAGCGGAGAACAACTACAAGACC 1170
Db 2497 CCCAGGACATCGCGTGGAGTGGAGAGCAANTGGCAGCGGAGAACAACTACAAGACC 2556
QY 1171 AGCGCTCCCGTCTGAGCTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACGCTGGAC 1230
Db 2557 AGCGCTCCCGTCTGAGCTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACGCTGGAC 2616
QY 1231 AAGAGCAGTGGCAGCAGGGAACTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCAC 1290
Db 2617 AAGAGCAGTGGCAGCAGGGAACTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCAC 2676
QY 1291 AACCCTACACGACAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 2677 AACCCTACACGACAGAGCCTCTCCCTGTCTCCGGGTAAATGA 2721
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RESULT 9

US-09-049-672A-21

; Sequence 21, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

```
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGSTUT11
CLONE: 2747531
US-09-049-672A-21
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Query Match 79.9%; Score 1066.4; DB 3; Length 1655;
Best Local Similarity 88.2%; Pred. No. 1.1e-244; Mismatches 136; Indels 24; Gaps 2;
Matches 1192; Conservative 0;

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QY 2 AGGTGCAGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 105 AGGTCCAGTTGTGTACAGTCTGGGCTGAGGTGAAGAGCCTGGGCTCAGTCAGGTCT 164
QY 62 CTTGTGCAGCTAGCGGATTCACCTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCTC 121
Db 165 CTTGCACGCTTTCGGGATTCACCTTCAGTGAATTTATCCGTGCACCTGGGTGCGACAGCTC 224
QY 122 CAGGGAAGGGCTCGAGTGGGTTGCTGAAATAGATGAAATCTGATAATATGTAACAC 181
Db 225 CTGGACAGGGCTTCAGTGGATGGAG-----GTTTAGCTCTGAAATGGAGGCGAG 278
QY 182 ATTATGGCGAGTCTGTGAAGGGGAAATTCACCTCTCAAGAGATGATTCAAAATCTAGAC 241
Db 279 TCTAGCACAGAAATTCCTGGCAGACTCACCTTGTCCGAGGACACACTCTGCAGACACAG 338
QY 242 TGTATCTGCAAAATGAACAGCCTGAAACCCGAGGACACACCGTGTATTACTGTACA---- 297
Db 339 CTTACATGTTTCTGAACAACCTAGGATCTGAGGACTCGGCCATCTATTACTGTCAAGAC 398
QY 298 -----GATTTTCATAGACTGGGCGCCAGGGAACACTAGTCAACCGCTCTCTCTCAG 343
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Db 1714 ACCGTCCTCTCGGCTCCACCAAGGCGCCATCGGTTCTCCCGCTGGCACCCCTCTCTCCAAAG 1773
QY 391 AGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 450
Db 1774 AGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 1833
QY 451 GTGACGGTGTCTGGAACTCAGCGCCCTGACACAGCGGCTGCACACCTTCCCGGCTGTC 510
Db 1834 GTGACGGTGTCTGGAACTCAGCGCCCTGACACAGCGGCTGCACACCTTCCCGGCTGTC 1893
QY 511 CTACAGTCTCTAGGACTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTG 570
Db 1894 CTACAGTCTCTAGGACTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTG 1953
QY 571 GGCACCCAGACCTTACATCTGCAACGTGAATCACAGCCCGACCAACCAAGGTGACACAAG 630
Db 1954 GGCACCCAGACCTTACATCTGCAACGTGAATCACAGCCCGACCAACCAAGGTGACACAAG 2013
QY 631 AAGTGGAGCCCAAACTTGTGACAAAACCTACACATGCCCGCCACCGTGCCTCCAGCAGCTGAA 690
Db 2014 AAGTGGAGCCCAAACTTGTGACAAAACCTACACATGCCCGCCACCGTGCCTCCAGCAGCTGAA 2073
QY 691 CTCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGTGACACAAGTGCATGATC 750
Db 2074 CTCGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGTGACACAAGTGCATGATC 2133
QY 751 TCCCGGACCCCTGAGGTACATGCTGCTGCTGAGTGGAGTGCAGCCAGCAAGACCCCTGAGTGC 810
Db 2134 TCCCGGACCCCTGAGGTACATGCTGCTGAGTGGAGTGCAGCCAGCAAGACCCCTGAGTGC 2193
QY 811 AAGTTCACCTGCTAGCTGACGCGCTGGAGTGCATATGCCAAGCAAAAGCCGGGGAG 870
Db 2194 AAGTTCACCTGCTAGCTGACGCGCTGGAGTGCATATGCCAAGCAAAAGCCGGGGAG 2253
QY 871 GAGCAGTACAAAGCAGCTACCGTGTGTCAGCGTCTCTCAGCGTCTCTGCAACGAGACCTGG 930
Db 2254 GAGCAGTACAAAGCAGCTACCGTGTGTCAGCGTCTCTCAGCGTCTCTGCAACGAGACCTGG 2313
QY 931 CTGAATGGCAAGGAGTACAAAGTGTCAAGGCTCTCAACAAAGCCCTCCAGCCCGCATCGAG 990
Db 2314 CTGAATGGCAAGGAGTACAAAGTGTCAAGGCTCTCAACAAAGCCCTCCAGCCCGCATCGAG 2373
QY 991 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAACCAAGGTGTACACCTGCCCCCA 1050
Db 2374 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAACCAAGGTGTACACCTGCCCCCA 2433
QY 1051 TCCCGGATGAGTGAACCAAGAACCAAGTGCAGCTGCTGCTGCTCAAGGCTTCTAT 1110
Db 2434 TCCCGGATGAGTGAACCAAGAACCAAGTGCAGCTGCTGCTGCTCAAGGCTTCTAT 2493
QY 1111 CCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCGAGCCCGGAGAACCAACTACAAAGACC 1170
Db 2494 CCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCGAGCCCGGAGAACCAACTACAAAGACC 2553
QY 1171 AGCCCTCCCGTGTGACTCCGAGCGCTCTCTTCTTCTTCTACAGCAAGTCAACCGTGGAC 1230
Db 2554 AGCCCTCCCGTGTGACTCCGAGCGCTCTCTTCTTCTTCTACAGCAAGTCAACCGTGGAC 2613
QY 1231 AAGAGCAGTGGCAGCAGGGAACGCTTCTCTATGCTCGGTGATCATGAGGCTCTGAC 1290
Db 2614 AAGAGCAGTGGCAGCAGGGAACGCTTCTCTATGCTCGGTGATCATGAGGCTCTGAC 2673
QY 1291 AACCCTACACGAGAGAGCCCTCTCTCTGCTCCGGGTAAATGA 1335
Db 2674 AACCCTACACGAGAGAGCCCTCTCTCTGCTCCGGGTAAATGA 2718
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RESULT 11

PCT-US95-09576-3
; Sequence 3, Application PC/TUS9509576
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING

; TITLE OF INVENTION: HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09576
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286740
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 798PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US95-09576-3

Query Match 79.7%; Score 1063.4; DB 5; Length 6557;
Best Local Similarity 88.3%; Pred. No. 8.3e-244;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;

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QY 1 GAGTGTGACGTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAATTTACGTGTGGAGTCTGGCGTGGCTGGTGCAGCCAGGGGGCTCCTCCGTTG 1422
QY 61 TCCTGTGACGTACCGGATTCACCTTCA---GTGGCTACTGGATGCTCTGGTCCGCCAG 117
Db 1423 TCCTGTGACGTTCCTGGCTACTCCATCACCTCCGGATATAGTGGAACTGGATCCGTCAG 1482
QY 118 GCTCCAGGAAGGGGCTCGAGTGGTGTCTGAAATAGATTGAAATCTGATATTATGCA 177
Db 1483 GCCCGGGTAAGGCCCTGGATGGGTGC-----ATCGATTAGTATGCCGGATCG 1533
QY 178 ACACATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237
Db 1534 ACTAATAATAACCTAGCTGCAAGGGCGGTATCACTATAAGTCGCGACGATTCCAAAC 1593
QY 238 AGACTGTATCTGCAAAATGACAGCTCAAAACCCAGACACACCCGTTGTTACTGTAC- 296
Db 1594 ACATTCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCGCTCTATTATTGTGCT 1653
QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAGTC 330
Db 1654 CGAGGCAGCCACTATTTCGGGCGCTGGCACTTCGCCGTGTGGGTCAAGAACCTTGCTC 1713
QY 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCACTGGTCTTCCCGCTGGCACCCCTCTCTCAAG 390
Db 1714 ACCGTCTCTCAGCCTCCACCAAGGGCCCACTGGTCTTCCCGCTGGCACCCCTCTCTCAAG 1773
QY 391 AGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTCTGCTCAAGGACTACTTCTCCCGAACCG 450
Db 1774 AGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTCTGCTCAAGGACTACTTCTCCCGAACCG 1833
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QY 451 GTGAGGCTGTCTGGAAGTCTAGGCGCCCTGACAGAGCGGTGCACACCTTCCCGGCTGTC 510
Db 1834 GTGAGGCTGTCTGGAAGTCTAGGCGCCCTGACAGAGCGGTGCACACCTTCCCGGCTGTC 1893
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTG 570
Db 1894 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTG 1953
QY 571 GGCACCCAGACCTATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTTGCAAG 630
Db 1954 GGCACCCAGACCTATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTTGCAAG 2013
QY 631 AAAGTGGAGCCCAATCTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 690
Db 2014 AAAGTGGAGCCCAATCTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 2073
QY 691 CTCGCGGGGCGACGCTCAGTCTTCTCTTCCCGCCCAAAACCCAGAGCACCTCATGATC 750
Db 2074 CTCGCGGGGCGACGCTCAGTCTTCTCTTCCCGCCCAAAACCCAGAGCACCTCATGATC 2133
QY 751 TCCCGGACCCCTGAGTGCATGCTGCTGTGTGACGTGAGCCAGCAAGACCTTGAGGTC 810
Db 2134 TCCCGGACCCCTGAGTGCATGCTGCTGTGTGACGTGAGCCAGCAAGACCTTGAGGTC 2193
QY 811 AAGTTCAACTGGTAGTGGACGCGCTGAGGTGCATATGCAAGACAAAGCCGCGGAG 870
Db 2194 AAGTTCAACTGGTAGTGGACGCGCTGAGGTGCATATGCAAGACAAAGCCGCGGAG 2253
QY 871 GAGCAGTACAACAGCAGCTACCGTGTGTGTGTCAGCTCTCCACCGTCTGACAGGACTGG 930
Db 2254 GAGCAGTACAACAGCAGCTACCGTGTGTGTGTCAGCTCTCCACCGTCTGACAGGACTGG 2313
QY 931 CTGAATGCCAAGGAGTACAAGTGAAGTCTCCCAAGAAAGCCCTCCAGCGCCCATCGAG 990
Db 2314 CTGAATGCCAAGGAGTACAAGTGAAGTCTCCCAAGAAAGCCCTCCAGCGCCCATCGAG 2373
QY 991 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGCAACAGGTGTACACCTGCCCCCA 1050
Db 2374 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGCAACAGGTGTACACCTGCCCCCA 2433
QY 1051 TCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCGTGTCAAAGGCTTCAT 1110
Db 2434 TCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCGTGTCAAAGGCTTCAT 2493
QY 1111 CCCAGGACATCGCGTGGAGTGGAGAGCAATGGGAGCCGCGAGCAACTACAAGACC 1170
Db 2494 CCCAGGACATCGCGTGGAGTGGAGAGCAATGGGAGCCGCGAGCAACTACAAGACC 2553
QY 1171 ACGCTCCCGTGTGCTGAGCTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGAC 1230
Db 2554 ACGCTCCCGTGTGCTGAGCTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGAC 2613
QY 1231 AAGAGCAGTGGCAGCAGGGAAGCTCTTCTATGCTCCGATGATGATGAGGCTCTGCAC 1290
Db 2614 AAGAGCAGTGGCAGCAGGGAAGCTCTTCTATGCTCCGATGATGATGAGGCTCTGCAC 2673
QY 1291 AACCACACAGCAGACAGCCTCCTCCTCTCCCGGGTAAATGA 1335
Db 2674 AACCACACAGCAGACAGCCTCCTCCTCTCCCGGGTAAATGA 2718
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RESULT 12

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US-08-378-939-9
; Sequence 9, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
```

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; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: gDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 35..92
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..1465
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..1465
; US-08-378-939-9
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Query Match 78.1%; Score 1042.6; DB 2; Length 1617;

Best Local Similarity 86.6%; Pred. No. 4.9e-234; Mismatches 139; Indels 51; Gaps 2;

Matches 1194; Conservative 0;

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QY 2 AGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 93 AGATGCAGGTGTGTCAGTCTGGGGCTGAAGTAAAGAGCCTGGTCTCTCGGTGACGGTCT 152
QY 62 CTTGTGCAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGTCTTGGTCCGCCAGGCTC 121
Db 153 CTTGCAAGGACTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCC 212
QY 122 CAGGGAAGGGCTCGAGTGGTGTGTAATAGATTGAATCTGATATTAATGTAACAC 181
Db 213 CTGGACAAGGCTTGTAGTGGTGGAG-----GGATATCCCTCTTTTGGTACACAA 266
QY 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 267 CCTACTCAGAACTTCCAGGGCAGAGTACCGATACCGCGACAAATCCACCACACAG 326
QY 242 TGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTACTACAG--- 298
Db 327 CCACATGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 386
QY 299 -----ATTTTCATAGACTGGGCC 316
Db 387 ATCGCTACAGGAGGCAAAATTTTGACCGGCGCGGGTGGGTGGTTCGACCCCTGGGCC 446
QY 317 AGGGAACACTAGTACCGCTCCTCCTCAGCCCTCCACCAAGGCGCCATCGGTCTTCCCCCTGG 376
Db 317 AGGGAACACTAGTACCGCTCCTCCTCAGCCCTCCACCAAGGCGCCATCGGTCTTCCCCCTGG 376
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Db 413 CGGAGTCTCGTTCACCGTCTCTCCTCAGTAGCACCAAGGGGCCCATCGGTCTTCCCCCTGG 472
Qy 377 CACCTCTCTCAAGACACCTCTTGGGGGACAGAGGGCCCTGGGTGCTGCTGCTCAAGACT 436
Db 473 CACCTCTCTCAAGACACCTCTTGGGGGACAGAGGGCCCTGGGTGCTGCTGCTCAAGACT 532
Qy 437 ACTTCCCGGAACCGGTGACGGTGTCTGGAACACTCAGGCGCCCTGACACAGGGGGTGCACA 496
Db 533 ACTTCCCGGAACCGGTGACGGTGTCTGGAACACTCAGGCGCCCTGACACAGGGGGTGCACA 592
Qy 497 CTTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 556
Db 593 CTTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 652
Qy 557 CTTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 616
Db 653 CTTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGC 712
Qy 617 CCAAGGTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAACTCACAACATGCCACCGT 676
Db 713 CCAAGGTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAACTCACAACATGCCACCGT 772
Qy 677 GCGGACGACCTGAACCTCGCGGGGACCGTCAAGTCTTCTTCTTCCCGCCCAAAACCCCAAG 736
Db 773 GCGGACGACCTGAACCTCGCGGGGACCGTCAAGTCTTCTTCTTCCCGCCCAAAACCCCAAG 832
Qy 737 ACACCTCTATGATCTCCGGGACCCCTGAGTTCACATCGGTGGTGGAGCTGAGCCACG 796
Db 833 ACACCTCTATGATCTCCGGGACCCCTGAGTTCACATCGGTGGTGGAGCTGAGCCACG 892
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Db 893 AAGACCTGAGGTCAAGTTCACCTGAGTTCACATCGGTGGTGGAGCTGAGCCACG 952
Qy 857 CAAGCCGCGGGAGGAGCAGTACACAGCAGTACCGTGTGGTGGAGCTGAGCCACG 916
Db 953 CAAGCCGCGGGAGGAGCAGTACACAGCAGTACCGTGTGGTGGAGCTGAGCCACG 1012
Qy 917 TGCACGAGGACTGCTGCTGAATGGCAAGGAGTACAAGTCAAGTTCACCAAGAGCCCTCC 976
Db 1013 TGCACGAGGACTGCTGCTGAATGGCAAGGAGTACAAGTCAAGTTCACCAAGAGCCCTCC 1072
Qy 977 CAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGAGCCAGCCCGGAGAACCCAGAGTGT 1036
Db 1073 CAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGAGCCAGCCCGGAGAACCCAGAGTGT 1132
Qy 1037 ACACCTGCCCCATCCCGGGATGAGTGAACCAAGAACCCAGGTCAGCCTGACCTGCTGG 1096
Db 1133 ACACCTGCCCCATCCCGGGATGAGTGAACCAAGAACCCAGGTCAGCCTGACCTGCTGG 1192
Qy 1097 TCAAGGCTTCTATCCAGCAGACATCCCGGTGGAGTGGGAGAGCAATGGGACGCGGAGA 1156
Db 1193 TCAAGGCTTCTATCCAGCAGACATCCCGGTGGAGTGGGAGAGCAATGGGACGCGGAGA 1252
Qy 1157 ACAACTCAAGACACGCTCCCGTGTGGACTCCGAGCGCTCTCTCTCTCTACAGCA 1216
Db 1253 ACAACTCAAGACACGCTCCCGTGTGGACTCCGAGCGCTCTCTCTCTCTACAGCA 1312
Qy 1217 AGCTCACCGTGGACAAGAGCAGTGGGAGCAGGGAACGCTTCTCTCATGCTCCGCTGATGC 1276
Db 1313 AGCTCACCGTGGACAAGAGCAGTGGGAGCAGGGAACGCTTCTCTCATGCTCCGCTGATGC 1372
Qy 1277 ATGAGGCTCTGCACACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 1373 ATGAGGCTCTGCACACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1431
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RESULT 14

US-08-793-450-7
; Sequence 7, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA

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; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHAABIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA USA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24.618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1418 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1418  
; FEATURE:  
; NAME/KEY: sig_peptide  
; LOCATION: 1..57  
; FEATURE:  
; NAME/KEY: mat_peptide  
; LOCATION: 58..1418  
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY  
; OTHER INFORMATION: CHAIN"  
; US-08-793-450-7
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Query Match 77.9%; Score 1039.8; DB 4; Length 1418;
Best Local Similarity 86.7%; Pred. No. 2.2e-238;
Matches 1187; Conservative 0; Mismatches 137; Indels 45; Gaps 2;

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Qy 2 AGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 AGGTCCAACTGGAGCAGTGGGGCGCAGGACTCTTGAAGCCTTCGGGAGACCTGTCCCTCA 118
Qy 62 CCTGTGCACGTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCTC 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 CTGTGCACTGTCTATGTGGGTCTCTTCAGTGGTACTTCTGAGCTGGAGCTGGATCCGCCAGCCCC 178
Qy 122 CAGGGAAGGGGCTCGAGTGGGTTCGCTGAAATTAGATTGAAATCTGATATTAATGCAACAC 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 CAGGGAAGGGGCTGGAGTGGATGGGAATCA-----ATCATAGTGAAGCACCA 229
Qy 182 ATTATCGGAGTCTGTGAAGGGGAAATTACCATCTCAAGAGATGATTCAAATCTAGAC 241
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Db 230 ACTACAACCCGCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACAGTCCCAAGAACCACT 289
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QY 242 TGTATCTGCAATGAACACGCTGAAACCCGAGGACACAGCGGTGATTACTGTACAGATT 301
DB 290 TCTCCCTGAACTGAACCTGTGACCGCGCGGACACGCGTGTGTATTTACTGTGGAGGG 349
QY 302 TCATAGA-----CTGGGGCCAGGGACAC 325
DB 350 CCCAGAGTATAAATGAAGTATCATGTTGGGACTGTTGACCCCTGGGGCCAGGTACCA 409
QY 326 TAGTCACGCTCTCCCTCAGCCTCCACCAAGGCCCCATCGTCTCCCTGCGCACCCCTCT 385
DB 410 CTGTACCGCTCTCCCTCAGCCTCCACCAAGGCCCCATCGTCTCCCTGCGCACCCCTCT 469
QY 386 CCAAGACACCTCTCTGGGGCAGCGGCTGGGCTGGTGGTCAAGACTACTTCCCG 445
DB 470 CCAAGACACCTCTCTGGGGCAGCGGCTGGGCTGGTGGTCAAGACTACTTCCCG 529
QY 446 AACCGGTGACGCTGTCTGGGAACCTCAGCGGCTGACAGGGGCTGACACCTTCCCG 505
DB 530 AACCGGTGACGCTGTCTGGGAACCTCAGCGGCTGACAGGGGCTGACACCTTCCCG 589
QY 506 CTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGAACCTGCCCTCCAGCA 565
DB 590 CTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGAACCTGCCCTCCAGCA 649
QY 566 GCTTGGCCACCCAGCCTACATCTGCAAGCTGAATCACAAGCCAGCAGCAACCAAGGTG 625
DB 650 GCTTGGCCACCCAGCCTACATCTGCAAGCTGAATCACAAGCCAGCAGCAACCAAGGTG 709
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DB 710 ACAAGAAAGTGAGGCCAAATCTTGTGACAAACTCACAATGCTGCCCGTGGCCAGGAC 769
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DB 830 TGATCTCCGGACCCCTCAGGTACATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 889
QY 806 AGGTCAAGTCAACTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 865
DB 890 AGGTCAAGTCAACTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 949
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DB 950 GGGAGGAGCAGTACACAGCAGTACCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1009
QY 926 ACTGGTGAATGGCAAGGAGTACAGTGGAGGTCTCCAAAGACCCCTCCAGCCGCCA 985
DB 1010 ACTGGTGAATGGCAAGGAGTACAGTGGAGGTCTCCAAAGACCCCTCCAGCCGCCA 1069
QY 986 TCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTGC 1045
DB 1070 TTGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACAGGTGTACACCTGC 1129
QY 1046 CCCATCCCGGATGAGTGTGCAAGAACACAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1105
DB 1130 CCCATCCCGGATGAGTGTGCAAGAACACAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1189
QY 1106 TCTATCCAGCAGATCGCGGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACACTACA 1165
DB 1190 TCTATCTAGCAGATCGCGGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACACTACA 1249
QY 1166 ACACACGCTCCCTGCTGGAATCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1225
DB 1250 AGACACGCTCCCTGCTGGAATCCGAGCGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1309
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RESULT 15
US-08-149-099C-3
; Sequence 3, Application US/08149099C
; Patent No. 5736137
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; APPLICANT: HANNA, Nabil
; APPLICANT: LEONARD, John E.
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: REFF, Mitchell E.
; APPLICANT: RASTETTER, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,099C
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 12-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-149-099C-3
Query Match 77.9%; Score 1039.8; DB 1; Length 9209;
Best Local Similarity 86.8%; Pred. No. 3.8e-238;
Matches 1181; Conservative 0; Mismatches 147; Indels 33; Gaps 2;
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Db 3773 ACTACACGCGAGAGAGCCCTCTCCCTGTCTCCGGTAAATGA 3813

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